Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

BLOSUM62

Scoring table:

US-09-972-032-2 456

Title: Perfect score:

Sequence:

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OM protein

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Run

length: 0 length: 2000000000

Minimum DB seq Maximum DB seq

Searched:

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99 Human PRO
11 Human CDN
12 Human CDN
2 Nevel hum
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2 Nevel hum
3 Human PRO
8 Human PRO
8 Human PRO
9 Human PRO
1 Human PRO
6 Novel hum
7 Human PRO
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7 Human PRO
7 Human PRO
8 Human PRO
9 Human PRO
9 Human PRO
1 Human CDN
6 Human CDN
6 Human CDN
1 Human PRO
             Ada43808 Human C
Ada401251 Human C
Ada401251 Human C
Ada40842 Human Cl
Ada60842 Human Cl
Ada60842 Human D
Adb997018 Human D
Adb997018 Human D
Adb99506 Novel D
Adb99506 Novel D
Adb99506 Novel D
Adb99507 Human Cl
Adc20455 Human Cl
Adc20418 Human DF
Adc11281 Human DF
Adc11281 Human DF
Adc11281 Human DF
Adc1281 Human DF
Adc1828 Human DF
Adc1828 Human DF
Adc1828 Human CC
Adc371 Human DF
Adc1828 Human CC
Adc371 Human DF
Adc182909 Human CA
Adc18291 Human CA
Adc1829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Estrogen Receptor Coregulator 3; ERCoA3; tamoxifen; estrogen; cancer; osteoporosis; cytostatic; osteopathic; human; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
/product= "ERCoA3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
 ADA01379
ADA43576
ADA435808
ADA43576
ADA01251
ADA01251
ADA06954
ADA0699735
ADB99735
ADB99851
                                                                                                                                                                                                                                                                                                              ADE51878
ADE37736
ADE37736
ADE37620
ADE38091
ADE39503
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ADE39504
ADE39769
ADE39769
ADE37347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
203. .442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human ERCoA3 protein encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYCA-) UNIV CASE WESTERN RESERVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL60606 standard; cDNA; 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-OCT-2001; 2001WO-US031271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-OCT-2000; 2000US-0238190P.
                                                                                                                                                                                                                                                                                                   10010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-AUG-2002 (first entry)
  Sutton A;
  WO200228352-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Montano M,
ABL60606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1
ABL60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
 Abl66666 Human ERC
Aas69040 DNA encod
Aac86940 Human GPC
Aad54213 Streptomy
Aad54217 Streptomy
Aaas20885 A. sulcat
Aah52281 Human AFP
AbK70016 cDNA enco
                                                                             July 10, 2004, 15:29:15; Search time 372 Seconds (without alignments) 902.171 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                        MCGRPRRVSAGCGFADAHWT......SAGLTVRDRPQLGELCMGRG
       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                       nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                        3373863 segs, 2124099041 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                             7.00.5
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AAS69040
ADC86940
AAD54223
AAD54217
AAA50885
AAH52281
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genesequ2001bs: genesequ2002s: genesequ2003as:* genesequ2003bs:* genesequ2003cs:*

geneseqn2004s:*

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DB

Length

Query Match

Score

Result No.

900077600

990 349901 24081 52101 696 943

100.0 36.1 20.7 20.7 20.7 20.5 20.5

16456 94 49 94 95 10 94 55 10 94 55 10 94 55 10 94 55 10 94 55

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Database

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(HYSE-) HYSEQ INC.
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DB:
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                                New polypeptide, that is a functional equivalent of ERCOA3 (Estrogen Receptor Coregulator 3), is useful in inhibiting or reducing tamoxifen or estrogen-induced proliferation of cancer cells and in treating
                                                                                                                                                                                                                                                                                                                                                               GGGCTCTGGACTGGGGCTAGGGGAAGGCCAGGAGGGGGGGAATTGGGCCCGAGGGCCAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         382
                                                                                                          The invention relates to a ERCOA3 (Estrogen Receptor Coregulator 3) protein and encoding polynucleotides. ERCOA3 can be used to inhibit or reduce tamoxifen or estrogen induced proliferation of cancer cells, by reduced activity of ERCOA3, and for detecting cancer cells that are tamoxifen resistant, or to treat osteoporosis, by increasing levels of ERCOA3 in cells. The encoding polynucleotide can be used to inhibit translation of a mRNA encoding ERCOA3. ERCOA3 acts as a coregulator protein and can bind to the estrogen receptor to activate a molecular or cellular response in the cell. The present sequence represents the human
                                                                                                                                                                                                                                                                                                                                                                                                           GlyLeuTrpThrGlyLeuGlyGluGlyGluGlyGluGlyGlyIleGlyProGluGlyGlnAla 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerProThrProAspCysAlaSerArgTrpProArgSerAlaSerArgTrpProTrpSer 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAGGICTTACCGTCCGAGATCGTCCGCAACTGGGCGAGCTGTGCATGGGGCGTGGC 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOGCOGACCOCCGACTGCGCCTCCCGGTGGCCCCCGCAGCGCCTCCCGGTGGCCCTGGGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AlaGlyLeuThrValArgAspArgProGlnLeuGlyGluLeuCysMetGlyArgGly
                                                                                                                                                                                                                                 Sequence 990 BP; 189 A; 281 C; 317 G; 203 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                DNA encoding novel human diagnostic protein #4844.
                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                        5; Fig 1; 39pp; English.
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AAS69040 standard; cDNA; 597
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23-AUG-2000; 2000US-00649167.
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456.00
100.00%
100.00%
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                                                                                                                                                                                                             ERCoA3 encoding cDNA
    WPI; 2002-454492/48
                                                                                                                                                                                                                                                                                                   Similarity:
               P-PSDB; ABB08035
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                                                                                                                                                                                                                                                                                        Percent Similarity:
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                                                                    osteoporosis
                                                                                                                                                                                                                                                         Alignment Scores:
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                                                                                        Claim
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed consistent of (II) is useful in gene therapy techniques to restore normal colypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of supplement. (II) and its binding partners are useful in medical imaging of supplement. (II) and its binding partners are useful in medical imaging of supplement. (II) and (II) and (II) and subject treating disorders in volving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in dispensible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amine and to produce other types of data and products dependent on DNA and coning sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this parent did not appear in the printed specification, but was obtained in the form of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        463
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                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -- ProThrProAspCys-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 597 BP; 97 A; 217 C; 196 G; 87 T; 0 U; 0 Other;
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 4844; 103pp; English.
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YT;
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Drmanac RT, Liu C,
                                                                    WPI; 2001-639362/73
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Best Local Similarity:
                                                                                                             P-PSDB; ABG04853
                                                                                                                                                                                                                                                                                           siodiversity.
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Pred. No.:
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us-09-972-032-2 1.rng

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x AAD54223 (1-24081)
 -LeuGlyGluLeuCysMet
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                   WO200288176-A2.
                                                                                                                                                                                                                                                   Streptomyces
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                                                                                                                                            17-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                               07-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Farnet CM,
71
                                                                                                                 AAD54223;
                                                                                                                                                                                                                                                                               Key
                                                                       AAD54223
                                                                                                   107127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106952 ACAAGCACCGCGCAGCCCTGGGTCCTGCCCACACCTCTCCCCACACCTCCCCGCAA 106893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107072 GCAGCTAAAGGCCTGGTGAGAAATCGAGCACAGCAGCTGCTGGCCCAGGTGCTAAGCCCCT 107013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel polynucleotide encoding a guanosine triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of the invention may have a use in gene therapy. The polynucleotide and polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor. The polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 349901 BP; 106873 A; 66040 C; 67419 G; 108968 T; 0 U; 601 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32
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                                                                                                                                                                                                                                                                                                                                                                              New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlyArgProArgArgValSerAlaGlyCysGlyPheAlaAspAlaHisTrpThrGlyLeu 22
                                                                 ds; gene; human; GPCR;
guanosine triphosphate-binding protein coupled receptor; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 ArgserAlaSerArgTrpProTrpSerAla---GlyLeuThrValArgAspArgProGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107177 GGCGGCACTCGTCGGCGAGACTTGGGCTGC-----GCAGGAGCCCACGGCAGTGGG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   349901
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 1393; 28pp; English.
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                                       Human GPCR gene SEQ ID NO:1393.
                                                                                                                                                                                                   18-JUN-2002; 2002EP-00013517.
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95.00
37.39%
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20.83%
          (first entry)
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P-PSDB; ADC86941.
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Best Local Similarity:
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                                                                                                                                          EP1270724-A2
                                                                                                             Homo sapiens
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The invention relates to novel proteins involved in the biosynthesis of polyketide dorrigocin (DORR) or lactimidomycin (LACT) biosynthesis by microorganisms. Sequences of the invention allow direct manipulation of dorrigocin, lactimidomycin and related chemical structures via chemical engineering of the enzymes involved in the biosynthesis of dorrigocin and lactimidomycin. They are useful for introducing chemical handles into normally inert positions that permit subsequence chemical modifications the invention can also be used to generate a focused library of analogues around a polyketide lead candidate to fine-tune the compound for optimal properties. They are useful for generating antibodies specific for the polyketide biosynthesis. The present sequence is Streptomyces platensis subspecies rosaccus DORR ORF6 DNA
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                                                                                                                                                                                                                                                                                                                                                                      Polyketide biosynthesis; dorrigocin; DORR; lactimidomycin; LACT; gene;
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1. 24081
7. 4tag= "
/product= "ORF6 protein"
/note= "No start codon"
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                                                                                                                                         BP.
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                                                                                                                                      AAD54223 standard; DNA; 24081
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P-PSDB; AAE35489.
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26-APR-2001; 2001US-0286346P.
26-APR-2002; 2002WO-CA000591
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Best Local Similarity:
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 SeralaGlyCysGlyPheAlaAspAlaHisTrpThrGlyLeuTrpThrGlyLeuGly-Gl 28
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                                                                 48 r------ArgTrpProArgSer-----AlaSerArgTrpPro---TrpSerAl
                                  28 uGlyGlnGluGlyGlyIleGlyProGluGlyGlnAlaSerProThrProAspCysAlaSe
                                                                                                                                                                                                 platensis subspecies rosaceus dorrigocin DNA
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009. .17587
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AAE35490, AAE35491, AAE35492, AAE35493.
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fluorescence resonance energy transfer; mutant; ss.
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ECOPIA BIOSCIENCES INC
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P-PSDB; AAE35484, AA
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cell;

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AAH52093 to AAH52303 encode the human secreted proteins given in AAG81242 to AAG81453. The secreted proteins can be used for directing the secretion of proteins of interest from a host cell including bacteria, fungal cells, and cultured higher eukaryotic cells. The present invention also describes fusion proteins, where a secreted protein of the invention is operably linked via a peptide bond or peptide linker to a second protein selected from the group consisting of maltose binding protein, an immunoglobulin constant region, a polyhistidine tag and a peptide given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CysGlyArgProArgArgValSerAlaGlyCysGlyPheAlaAspAlaHisTrpThrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated polypeptide for directing secretion of proteins of interest a host cell including, e.g. bacteria, includes contiguous amino acid residues of polypeptide with specified amino acids.
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                                                                                                 cell; fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 LeuTrpThrGlyLeuGlyGluGlyGlnGluGlyGlyIleGlyProGlu-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 A; 198 C; 205 G; 110 T; 0 U; 0 Other;
                                                                     Human AFP protein encoding cDNA sequence SEQ ID NO:377
                                                                                             Human, secreted protein, secretion, bacterial cell, eukaryotic cell; fusion protein; maltose binding primmunoglobulin constant region; polyhistidine tag;
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Matches:
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Local Similarity:
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P-PSDB; AAG81430
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                                            10-SEP-2001
                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is the coding sequence for humanised mutant fluorescent protein, Mutl, from non-bioluminescent Anemonia sulcata. The fluorescent protein has applications in fluorescent labelling, as fluorescent markers for gene expression and protein localisation studies, and in fluorescence resonance energy transfer (FRET) reactions. The coding sequence may be used as a source or primers and probes for identifying related proteins
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Best Local Similarity:
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 sulcata
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09-DEC-1999;
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recombinant means and antibodies specific for the protein of the invention. The antibody may be used for detecting the FRO proteins of the invention and may be used to modify their activity. Polyucleocides may be used to solate or a cDNA library to isolate the full-conference in the solate other cDNA, to construct hybridisation probes for a cDNA library to isolate the full-conference or malysis of individuals with genetic disorders, in assays to identify other proteins or molecules involved in binding reaction, to generate transgenic animals or knock-out animals which in turn are useful in the conference identification, and tissue typing. The PRO polypeptides are useful in gene therapy, and as molecular weight markers for protein electrophoresis purposes. The sequences may also be used to detect overexpression on PRO polypeptides in concerous tumours and for screening for differentially expressed genes using microarray technology. The present sequence represents a cDNA encoding a human PRO protein of the
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                    326 GGTCACCGCAGGCTCACCTTCCTGGGGCTGGTGGGCTGCCCTGCTGTCAC 385
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                                                                                                                 66 gAspArgProGlnLeu------GlyGluLeuCysMe
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Wood WI, Zhang Z;
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Stephan J, Watanabe CK,
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22-SEP-2000; 2000US-0230621P.
22-SEP-2000; 2000US-0231621P.
10-NOV-2000; 2000US-023147P.
112-JAN-2001; 2001US-0261878P.
16-JAN-2001; 2001US-0261939P.
16-JAN-2001; 2001US-0261939P.
16-JAN-2001; 2001US-026431P.
22-JAN-2001; 2001US-026431P.
23-FEB-2001; 2001US-026421P.
28-FEB-2001; 2001US-026421P.
28-FEB-2001; 2001US-026431P.
28-FEB-2001; 2001US-026431P.
28-FEB-2001; 2001US-026431P.
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04-APR-2001; 2001US-0282199P.
09-MAY-2001; 2001US-0290589P.
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01-JUN-2001; 2001WO-US017800
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2001WO-US021735
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Smith V,
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29-JUN-2001;
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Fong S;
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431

96

------GlyGluLeuCysMe

99

251

943 36 7 31 48 6

311

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44

-----GlyGlnAlaSerProThrPro

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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for proliferation or differentiation of chondrocyte cells and a method for clecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, cervical and liver tumours). The polypucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polymucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation and for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumantoid arthritis. This sequence represents a human PRO polymucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for stimulating proliferation of human microvascular endothelial cells, and PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
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Zhang 7
rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.
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Wood WI,
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Watanabe CK,
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Stephan JP,
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18-JUL-2002; 2002US-00197942.
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Smith V,
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                                         Homo sapiens.
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Gurney AL,
Fong S;
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rérideceada controcada a respectado de controcado de controcado de controcado de controcado de controcado de controcado de contro de controcado de contro de 37 21 --GlyGlnAlaSerProThrPro 44 CysGlyArgProArgArgValSerAlaGlyCysGlyPheAlaAspAlaHisTrpThrGly LeufrpfhrGlyLeuGlyGluGlyGluGlyGlyIleGlyProGlu--Conservative: Mismatches: Indels: Length: Matches: x ADA01379 (1-943) 35.25% 29.51% 20.50% 93.50 Percent Similarity: Best Local Similarity: US-09-972-032-2 (1-79) Alignment Scores: 138 198 N Query Match: 셤 엄 ò à ò

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The invention relates to an isolated secreted/transmembrane (PRO) polypeptide, having at least 80% sequence identity to a sequence selected from any one of the 57 amino acid sequences given in specification, or to a sequence encoded by a nucleic acid molecule selected from any one of the nucleic acids deposited under any of the ATCC accession numbers given in specification, or a sequence having at least 80% identity to PRO with or without its associated signal peptide, an extracellular domain of PRO with or without its associated signal peptide. Also included are vectors, transformed host cells, anti-PRO antibodies, the nucleic acids encoding PRO, PRO fusion proteins, inducing endothelial cell tube formation (by administering PRO281, PRO150, PRO189, PRO4499, PRO6308, PRO6500, PRO1207, PRO1207, PRO250933 or PRO34274 polypeptide or its agonist) and
252 ACGCACATGACTGTGAGGCGCTGGGGCTCCGAGGCAGCAGCAGCTTCCAGGAGTCCC 311
                                                                      :::
GAGGCACCGTCAAACTGCAGTTCGACATGATGCGCGCCTGCAACCTGGTGGCCACGGCCG 371
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in
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                                                  ----TrpProArg---
                                                                                                                                                                                         -----GlyGluLeuCysMe
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Wood WI, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ss; gene; human; PRO; secreted protein; transmembrane protein; endothelial cell tube formation; chondrocyte cell differentiation; microvascular endothelial cell; tumour; lung tumour; celon tumour; prostate tumour; prostate tumour; rectal tumour; kidney tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cDNA encoding secreted/transmembrane polypeptide PRO21434
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Watanabe CK,
                                                45 Asp-----CysAlaSerArg----
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Stephan JP,
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liver tumour; cytostatic; vaccine
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18-JUL-2002; 2002US-00197942
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Smith V,
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P-PSDB; ADA43809.
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Fong S;
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an oligonucleotide probe derived from any one of the above nucleotide sequences. PRO6018 polypeptide is useful for stimulating the proliferation of differentiation of condroyer cells. PRO1313, PRO20080 and PRO6138 polypeptides are useful for stimulating the proliferation of human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006 to polypeptides are useful for inhibiting the proliferation of human microvascular endothelial cells. PRO 6071, PRO4487 and PRO6006 detecting the presence of tumour in a mammal, including tumours of lung, colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560, PRO189, PRO6499, PRO6508, PRO6000, PRO10275, PRO21207, PRO2031 and PRO34274 polypeptides are useful for inducing endothelial cell tube formation. PRO or the antibody are useful in the preparation of a medicament for treating a condition responsive to PRO polypeptide. The oligonucleotide probes are useful for isolating genomic and cDNA uncleotide probes, for measuring or detecting the expression of an associated gene, and as antisense probes. PRO nucleic acid is useful as hybridisation probe, in chromosome and gene mapping, in the generation of present sequence are useful as therapeutic agents, e.g. vaccines. The present sequence arecades a PRO protein. 197 312 GAGGCACCGTCAAACTGCAGTTCGACATGATGCGCGCCTGCAACCTGGTGGCCACGGCGG 371 372 cecrcaccecaeccaecricacericaceridenceiaecridenceecerecererereren 431 432 CCGACGCCCCGTGCGAGGAGGAGGCCATGCCGCTGCATTCCAACTGGCGAGTTTTGTCC 491 198 TGGTGGACGGGACCCGGGGAGGGCCGA-----GCCCTGGGGCCAGAGCCGGCCAGGTGG 251 25 37 44 ------SerAlaSerArgTrpProTrpSerAla-GlyLeuThrValAr 66 gAspArgProGlnLeu------GlyGluLeuCysMe 76 CysGlyArgProArgArgValSerAlaGlyCysGlyPheAlaAspAlaHisTrpThrGly -----GlyGlnAlaSerProThrPro ---TrpProArg--ss; gene; human; PRO; secreted protein; transmembrane protein; endothelial cell tube formation; chondrocyte cell differentiation; Human cDNA encoding secreted/transmembrane polypeptide PRO21434. Sequence 943 BP; 152 A; 306 C; 299 G; 186 T; 0 U; 0 Other; LeuTrpThrGlyLeuGlyGluGlyGluGlyGlyIleGlyProGlu-943 7 31 31 6 Length:
Matches:
Conservative:
Mismatches:
Indels: CysAlaSerArg-----US-09-972-032-2 (1-79) x ADA43808 (1-943) ADA43576 standard; cDNA; 943 93.50 35.25% 29.51% 20.50% (first entry) Asp----Percent Similarity: Best Local Similarity: TĠĠT 495 77 tGly Alignment Scores: 20-NOV-2003 22 23 26 ADA43576; 38 45 99 492 Query Match: DB: RESULT 11 ADA43576 à g g g g 음 g EXXXXXXXXXXX $\overset{\sim}{\circ}$ ò ò g ò ò à

New secreted and transmembrane PRO polypeptides, e.g. PRO20080 or PRO21383 useful for stimulating the proliferation or differentiation of chondrocyte cells and detecting the presence of a tumor in a mammal. PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The Grimaldi JC; Wood WI, Zhang Z; microvascular endothelial cell; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; kidney tumour; liver tumour; cytostatic; vaccine. Goddard A, Watanabe CK, present sequence encodes a PRO protein. Filvaroff E, Stephan JP, Claim 2; Fig 111; 307pp; English. .8-SEP-2002; 2002US-00246210. 04-APR-2001; 2001US-0282199P. 29-AUG-2001; 2001WO-US027099. 18-JUL-2002; 2002US-00197942. Eaton DL, F Smith V, S (GETH) GENENTECH INC. WPI; 2003-743814/70. P-PSDB; ADA43577 US2003073196-A1. Homo sapiens. 17-APR-2003. Gurney AL, Fong S; Baker KP,

Sequence 943 BP; 152 A; 306 C; 299 G; 186 T; 0 U; 0 Other;

Length: Matches: Conservative: Mismatches: Indels:

93.50 35.25% 29.51% 20.50%

Percent Similarity: Best Local Similarity: Query Match:

Pred. No.: Score:

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2; Fig 111; 308pp; English.
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T. Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated PRO polypeptides e.g. PRO281 and PRO1560, useful in preparation of a medicament for treating a condition responsive to polypeptide, and as therapeutic agents e.g. vaccines.
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Wood WI,
                                                                                                                22 LeufrpihrGlyLeuGlyGluGlyGluGlyGlyIleGlyProGlu-
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Watanabe CK,
         US-09-972-032-2 (1-79) x ADA43576 (1-943)
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Stephan JP,
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99US-0162506P.
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2001WO-US027099
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Smith V,
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29-OCT-1999;
02-DEC-1999;
29-AUG-2001;
18-JUL-2002;
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Fong S;
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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the projection or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. lung, colon, breast, prostate, rectal, kidney and liver tumoure). The polymucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antiense RNA and DNA and incommended and pene mapping, in generating entier.

CC polypeptides by recombinant techniques and in generating either can animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such a tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells and for inducing endothelial cell tube incomment.
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Conservative:
Mismatches:
Indels:
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93.50
35.25%
29.51%
20.50%
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The invention relates to an isolated secreted/transmembrane (PRO)

polypeptide, having at least 80% sequences identify to a sequence selected

from any one of the 57 amino acid sequences given in specification, or to

a sequence encoded by a nucleic acid molecule selected from any one of

the nucleic acids deposited under any of the ATCC accession numbers given

concerning its associated signal peptide, an extracellular domain of PRO

lacking its associated signal peptide, Also included are vectors,

transformed host cells, anti-PRO antibodies, the nucleic acids encoding

proportion proteins, inducing endochelial cell tube formation (by

administering PROSIS, PROSISS, PROSISS, PROSISS, PROSIOS, PROSIOSO,

proliferation or differentiation of chondrocyte cells. PROSISS,

an oligonucleotide probe derived from any one of the above nucleotide

proliferation or differentiation of chondrocyte cells. PROSISS,

and pROSISS polypeptides are useful for stimulating the proliferation of

proliferation of differentiation of chondrocyte cells. PROSISS,

and pROSISS polypeptides are useful for stimulating the proliferation of

microvascular endothelial cells. PROSON, PROSON,

polypeptides are useful for inhibiting the proliferation of human

microvascular endothelial cells. PROSON, PROSON,

proputides are useful for inhibiting the proliferation of human

microvascular endothelial cells. PRO polypeptides are useful for

medicament for treating a condition responsive to PRO polypeptide. The

colon, breast, prostate, rectal, kidney and liver. PROSEN,

PROSEN, PROSEN, PROSEN, PROSEN, PROSEN, PROSENT, PROSENT,

prostate, prostate, rectal, kidney and liver. PROSEN,

prostate, prostate, rectal, kidney and liver proparation of a

molectide sequences, for masuring or detecting the expression of a

nucleotide sequences, for masuring or detecting the expression of a

nucleotide sequences, for masuring or detecting the expression of a

nucleotide sequences probes. PROSENT, PROSENT, PROSENT, PROSENT, PROSENT, PROSENT, PROSENT, PROSENT, PRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grimaldi JC;
Wood WI, Zhang Z;
ss; gene; human; PRO; secreted protein; transmembrane protein; endochelial cell tube formation; chondrocyte cell differentiation; microvascular madothelial cell; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; kidney tumour; liver tumour; cytostatic; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baker KP, Eaton DL, Filvaroff E, Goddard A, Gurney AL, Smith V, Stephan JP, Watanabe CK, Fong S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Fig 111; 307pp; English.
                                                                                                                                                                                                                                                                                                                               02-AUG-2000; 2000US-0222695P.
20-UUN-2001; 2001WO-US019692.
29-AUG-2001; 2001WO-US027099.
18-JUL-2002; 2002US-00197942.
                                                                                                                                                                                                                                                                                    16-SEP-2002; 2002US-00245143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-625485/59.
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                                                                                                                                                                                         US2003068780-A1.
                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                        10-APR-2003
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Sequence 943 BP; 152 A; 306 C; 299 G; 186 T; 0 U; 0 Other;

Length: Matches: Conservative:

114 93.50 35.25%

Percent Similarity:

Alignment Scores:

HILIXBXHHHHHHHHHHHKRXHXHXRXHXHXHXHXHXHXHXHXHXH	est Local Similarity: 29.51% Mismatches: 31 Locry Match: 20.50% Indels: 48 B: Gaps: 6	-09-972-032-2 (1-79) x ADA01135 (1-943	2 CystyArgeroalgargvaseratery (22 LeuTrpThrGlyLeuGlyGluGlyGlnGluGlyGlyIleGlyProGlu 37 198 TGGTGGACAGGACCGGGGAGGGCGAGCCCTGGGGCCAGAGACGGCCAGGTGG 251	38	45 AspCyslaserys	::: 312 GAGGCACCGTCAAACTGCAGCATGATGATGCGCGCCTGCAACCTGGTGGCCACGGCCG 371	53SeralaSerArgTrpProTrpSerAla-GlyLeuThrValAr 66 372 GGTCACGGGAGGCCAGGTCACCTTCCTGGGGCTGGTGGGCCTGCTGTCTGT	66 gAspargProGlnLeu	 432 ccaacacccccaacaacaagaccaacaccactacattccaact	, 76 tGly 77	o 492 TGCT 495	RESULT 14 ADA43692 ID ADA43692 standard; cDNA; 943 BP. AC ADA43692;	20-NOV-	t Human cDNA encoding secreted/transmembrane polypeptide PR021434.	ss; gene; human; PRO; secreted protein; transmembrane protein; endothelial cell tube formation; chondrocyte cell differentiation; microvascular endothelial cell; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; kidney tumour; y liver tumour; cytostatic; vaccine.	Homo sapiens.	US2003073190-A1.	17-APR-2003.	9-SEP-2002; 2002US-00238283.	7 01-JUL-1998; 98US-0091358P. 7 02-JUN-1999; 99WO-US012252. 7 20-JUL-1999; 99US-0144758P. 7 25-JUL-1999; 99US-01313. 8 30-MAR-2000; 2000WO-US008439.	02-JUN-2000; 29-AUG-2001; 18-JUL-2002;	(GETH) GENENTECH INC.	<pre>I Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC; I Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z; I Fong S;</pre>
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372 CGCTCACCGCAGGCCAGCTCACCTTCCTCCTGGGGCTGGTGGGCCTGCCCCTGCTGTCAC 431

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New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or PRO21383, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy.
                         Claim 2, Fig 111; 352pp; English.
   WPI; 2003-585304/55.
      P-PSDB; ADA43693
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Sequence 943 BP; 152 A; 306 C; 299 G; 186 T; 0 U; 0 Other;

present sequence encodes a PRO protein.

			21	197	37	251	44	311	25	371	99
943 36 7	8 7		CysGlyArgProArgValSerAlaGlyCysGlyPheAlaAspAlaHisTrpThrGly	 CTGTGGAGGTCCTGCTGGC	VProGlu	GCCAGGTGG	GlyGlnAlaSerProThrPro 44	-0 -0	TrpProArg	GAGGCACCGTCAAACTGCGACTTCGACATGATGCGCGCCTGCAACCTGGTGGCCACGACGACGAACAAAAAAAA	SerAlaSerArgTrpProTrpSerAla-GlyLeuThrValAr 66
	. W 4. A		eA1	9000	661	-05 -05 -05 -05	G1	3GCA	!	TGC	-Se
Length: Matches: Conservative:	Mismatches: Indels: Gaps:	2 (1-943)	ValSerAlaGlyCysGlyPh	 TGTGCCAGACGCTGGAGGATGGCGCAGGCGTGGGGGCTGTGGAGGTCCTGCTGGC	22 LeuIrpIhrGlyLeuGlyGluGlyGlnGluGlyGlyIleGlyProGlu	BAGGGCGAGCCCT		SECTGGGCTGGGGCTCCGAG	CysAlaSerArg	AGTTCGACATGATGCGCGCC	SerAlaSerArgTrpProTr
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93.5	29.51% 20.50% 8	k AD	ProA	IGCT	31 y Le	3GAC	1	ACTG		rcaa.	; ; ;
res: aritv:	nilarity:	-2 (1-79)			LeuTrpThr			ACGCACATG	Asp		
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Alignment Scores: Pred. No.: Score: Percent Similarity	Best Local Similarity: Query Match: DB:	US-09-972-032-2 (1-79) x ADA43692 (1-943)	۵.	Db	δλ	qa	ζ,	qa	Qy	qq	δλ

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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The transmembrane polypeptides and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondroove cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, cervical and liver tumours). The polymucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polymucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a
                                                                                                                                                                                                                                                                                                                                                   Human, PRO; gene, ss; secreted polypeptide, transmembrane polypeptide, tumour necrosis factor-alpha, TNF-alpha; blood, chondrocyte cell; tumour; adrenal, lung; colon; breast, prostate; rectum; cervix; liver; microvascular endothelial cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; cartilage, sports-related joint problem; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemacollobin-associated disorder; thalassaemia; immune system cell infiltration; cancer; vulnerary; antianaemic; osteopathic; antirheumatic; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel secreted and transmembrane polypeptides, PRO polypeptides useful for stimulating proliferation or differentiation of chondrocyte cells and inducing endothelial cell tube formation.
                                   96
  ------GlyGluLeuCysMe
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Wood WI, Zhang Z;
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Watanabe CK,
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Smith V, Stephan JP, 1
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                                                                                                                                                                                               ADA06954 standard; cDNA; 943 BP
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15-MAY-2000; 2000WO-US01358.
29-AUG-2001; 2001WO-US027099.
18-UUL-2002; 2002US-00197942.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-SEP-2002; 2002US-00245771
                                                                                                                                                                                                                                                                                                                  Human PRO polynucleotide #56
gAspArgProGlnLeu--
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                                                                                                                  492 TGGT 495
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Fong S;
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medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for inducing endothelial cell tube formation and for treating various bone and/or cartilage disorders such as sports injuries and arthritis. PRO polypeptides which stimulate the release of proteoglycans from cartilage are useful for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO polypeptides are also useful for treating various mammalian haemoglobin-associated disorders such as various thalasseamias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence represents a human PRO polynucleotide of the invention.
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Sequence

943 36 11ve: 7 es: 48 6	CysGlyArgProArgArgValSerAlaGlyCysGlyPheAlaAspAlaHisTrpThrGly 21 	1ydlylleglyProglu 37 	GlyGlnAlaSerProThrPro 44 ACGACATGACTGTGAGGCTGGGCTCCGAGGCACCGGCTTCCAGGAGTCCC 311	Asp		gaspargproglnLeu	
114 Length: 33.55 Matches: 35.25\$ Conservative 29.51\$ Mismatches: 20.50\$ Indels: x ADA06954 (1-943)	gProArgArgValSerAlaGlyCys 	LeuTrpThrGlyLeuGlyGluGlyGluGlyGlyGlyIleGlyProGlu TGGTGGACGCGGGAGGCCGAGCCCTGGGGCCAAGCCG	GACTGTGAGGCGCTGGGCT	CysAlaSerArg ::: GTCAAACTGCAGTTCGACATGATGG	SerAlaSerArgTrr 	gAspargProg1nLeu	
Alignment Scores: Pred. No.: Score: Score: Becrent Similarity: Best Local Similarity: Desty Match: Best US-09-972-032-2 (1-79) x ADA06954	Oy 2 CysGlyAr 	Oy 22 Leurrpih Db 198 TGGTGGAC	Oy 38 Db 252 ACGCACAT	Oy 45 Asp ::: Db 312 GAGGACO	Oy 53 Db 372 CGCTCACC	Qy 66 gAspArgP Db 432 CCGACGCC	Oy 76 tGly 77 Db 492 TGGT 495

Search completed: July 10, 2004, 16:58:44 Job time: 452 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:

July 13, 2004, 08:38:15; Search time 2883 Seconds (without alignments) 818.284 Million cell updates/sec

US-09-972-032-2

1 MCGRPRRVSAGCGFADAHWT.....SAGLTVRDRPQLGELCMGRG 79 Title: Perfect score: Sequence:

Scoring table:

OLIGO Xgapop 60.0 , Xgapext 60.0 Ygapop 60.0 , Ygapext 60.0 Fgapop 60.0 , Pgapext 7.0 Delop 6.0 , Delext 7.0

Word size:

27513289 segs, 14931090276 residues

Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

55023952

Post-processing: Listing first 45 summaries

Command line parameters:
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-O-fcgn2_1/USFVO_sprool/VG09972032/runat_06072004_121534_0884/app_query.fasta_1.263
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -GTART=1 -END=-1 -MATRIX=0.11G0 -TRANS=human40.cd1 -LIST=45
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-NORM==xt -HEAPSIZES=500 -MAXLENS=20000000000.
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-DBV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
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gb_gss2:* 29:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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SUMMARIES DB ID	1 1 1 1 1 1	1 BC03950	3 BU62042	3 BX40613	2 BM6/95/	AMBROAD CHORDAD	3 BU61733	4 CA31314	4 CD74258	3 BQ447	A BESCOLO	4 R86559	AA65669	AA59354	AI022772	3 BU40576	3 BU11385	3 BU40337	3 BU354	0 BE62189	0 BF16813	8 AZO9978	4 W30123	3 BQ761	8 BH22343	9 CE01756	0 BB2934	9 CE66040	AI005741	8 ACLIS/0	BF7210	3 BQ80761) BF65162	DEFULZ24	DE71772) BE83770	14 CD810225 10 BE837692		ALIGNMENTS			1467 DP TRNA PIMAGE:5555626, TRNA	58499	-	,	; Chordata; Craniata; Primates; Catarrhi	7)
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                                                                             WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ArC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
WED site:
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BU620427
UI-H-FLI-bfw-n-19-0-UI.SI NCI CGAP_FLI Homo sapiens CDNA clone
UI-H-FLI-bfw-n-19-0-UI 3', mRNA sequence.
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Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 691)
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   Direct Submission
Submitted (01-WOV-2002) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LiML at: http://image.llnl.gov Series: IRAK Plate: 88 Row: g Column: 1 This clone has the following problem: retained intron. Location/Qualifiers
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Matches:
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/mol_type="mRNA"
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/clone="UT-E-E00-aia-1-05-0-UI"
/tissue_type="fetal eye"
/dev stage="fetal"
/lab host="Diffetal"
/lab host="Diffet
                                                                                                                                                                                                  Coordinated Laboratory for Computational Genomics
University of Lowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soaresœuiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.research.com).
Seq primer: M13 Forward
POLYA=Yes.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                           Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate
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97044477
8889548
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Genoscope - Centra National de Sequencage
Genoscope - Centra National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8395.f For
more information about this cluster, see
http://www.genoscope.cns.fr,
cgi.bin/cluster.cg?seq-CSOAM010CB10NP1&cluster=8395.f. Contact :
Feng Liang Email: fliang@lifetech.com URL :
http://tullangh.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOAM010CB10NP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dev stage="fetal"

"Cone lib="Homo sapiens FETAL LIVER"

/note="Organ: liver; Vector: pCWVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     614 ATTGG-CCCGAGGGCCAGGCCTCGCCGACCCCCGACTGCGCCTCCCCGGTGGCCCCCGCAGC 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23
                                                                                         Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full.length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaSerArgTrpProTrpSerAlaGlyLeuThrValArgAspArgProGlnLeuGlyGlu 73
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  GI:30648317
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us-09-972-032-2.rst

RESULT 5 BU684594/c LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

REFERENCE AUTHORS TITLE

MEDLINE PUBMED COMMENT JOURNAL

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Genome Res. 6 (9), 791-806 (1996)
US-09-972-032-2 (1-79) x BU684594 (1-694)
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//clone lib="UJ-CF-ENI"
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UJ-CF-ENI is a normalized cDNA library containing the following tissue(s): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-866,
1996. First strand CDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA as ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CTGCTCAGGT.
TAG IISSUE=Human Lung Epithelial Cell Lines untreated LPS GNT TAG LIB-UJ-CF-ENI
TAG_SEQ-CTGCTCAGGT"
                     BU684594 694 bp mRNA linear EST 07-OCT-2002 UI-CF-EN1-act-a-22-0-UI.SI UI-CF-EN1 Homo sapiens cDNA clone UI-CF-EN1-act-a-22-0-UI3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: Double and and a first part of Iowa Tissue Procurement: Dr. M. J. Welsh, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems Seq primer: M13 FORWARD POLYA-YES.
                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 694)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   University of Iowa Volstans, Iowa City, IA 52242, USA 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA Tel: 319 356 4666 Fax: 319 356 7171
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Conservative:
Mismatches:
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100.00%
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Pred. No.:
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FEATURES

Score:

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UI-CF-ENI is a normalized cDNA library containing the following tissue(s): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an oligo-GT primer containing a Not I site. Double stranded CDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CTGCTCAGGT.
TAG TISSUE=Human Lung Epithelial Cell Lines untreated LPS 6hr To LPS 24h
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University of Iowa Med Labs, Iowa City, IA 52242, USA
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Glone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
Seq primer: M13 FORWARD
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                       BM980506 760 bp mRNA linear EST 21-FEB-2003 UI-CF-EN1-add-a-08-0-UI.SI UI-CF-EN1 Homo sapiens cDNA clone UI-CF-EN1-add-a-08-0-UI 3', mRNA sequence.
                                                 Homo sapiens Sukaryota, Chordata; Craniata; Vertebrata; Euteleostomi; Mukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. 1 (bases 1 to 760)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
46 CysAlaSerArgTrpProArgSerAlaSerArgTrpProTrpSerAlaGlyLeuThrVal 65
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/mol type="mRNA"
/db_xref="taxon:9606"
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/clone="UI-CF-EN1-add-a-08-0-UI"
/clone="Primary Lung Cystic Fibrosis Epithelial
/cells"
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CA313142/c
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/ organism="Memo sapiens"
/ follor="mRAN"
/ follor="mRAN"
/ db xref="taxon:9606"
/ db xref="taxon:9606"
/ db xref="taxon:9606"
/ clone="UI-H-DF0-bep-n-09-0-UI"
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/ dev stage="Adult Life Technologies"
/ dab_host="Adult CGAP DF0"
/ lone lib="NOI CGAP DF0"
/ clone lib="NOI CGAP DF0"
/ cot contains the following tissue(F): Subchondral Bone. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BUG17331 632 bp mRNA linear EST 23-SEP-2002 UI-H-DF0-bep-n-09-0-UI.S1 NCI CGAP_DF0 Homo sapiens CDNA clone UI-H-DF0-bep-n-09-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                          53
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                 34 IleGlyProGluGlyGlnAlaSerProThr-ProAspCysAlaSerArgTrpProArgSe
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0 20
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Matches:
Conservative:
Mismatches:
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TAG_LIB=UI-CF-EN1
TAG_SEQ=CTGCTCAGGT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTGTGCATGGGGCGTGGC 535
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BU617331.1 GI:23283539
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                                                                                            2.66e-20
34.00
97.01%
97.01%
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Homo sapiens (human)
Homo sapiens
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Unpublished (1997)
                                                                                                                                 Percent Similarity:
Best Local Similarity:
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University of Iowa
University of Iowa Med Labs, Iowa City, IA 52242, USA
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
Seg primer: M13 FORWARD
POLYA=Yes.
with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT733-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The Equence tag for this library is GTAAAGCGTC.

TAG_TISSUE-subchondral bone
TAG_ESQ-GTTAAAGCGTC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CA113142 633 bp mRNA linear EST 04-NOV-2002 UI-CF-FN0-aex-n-23-0-UI.sl UI-CF-FN0 Homo sapiens cDNA clone UI-CF-FN0-aex-n-23-0-UI 3', mRNA sequence.
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/lab_hogt="DH10B (Life Technologies) (T1 phage resistant)"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 633)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47 AlaSerArgTrpFroArgSerAlaSerArgTrpFroTrpSerAlaGlyLeuThrValArg
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Matches:
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Best Local Similarity:
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AUTHORS
TITLE
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/dev_stage="Adult"
/dev_stage="Adult"
/lab host="DH10B (Life Technologies)"
/clone_lib="NCI_GAP_FT2"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_GAP_FT2 is a subtracted cDNA library constructed from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CD742581 623 bp mRNA linear EST 26-JUN-2003 UI-H-FT2-bjl-i-10-0-UI.S1 NCI CGAP_FT2 Homo sapiens cDNA clone UI-H-FT2-bjl-i-10-0-UI 3', mRNA sequence.
           /note=_organ: Lung/ Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; modified polylinker; Site 1: EcoR I; Site 2: Not I; U-CF-FNO is a subtracted cDNA library derived from two normalized Human lung epithelial cell libraries (ENI and DUI) The library was subtracted according to according to Bohaldo, Lennon and Soares, Genome Research, 6:791-806, bento-soares@ulowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
thtp://genome.uiowa.edu/distribution/cgap.html
Seg primer: M13 FORWARD
POLYA-Yes.
                                                                                                                                                                                       TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS 6hr to LPS 24h
TAG_LISEUL-CF-RNO
TAG_EBU-CTCAGGT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    633 GCCTCCCGGTGGCCCCGCAGCGCCTCCCGGTGGCCCTGGAGTGCTAGCCGTCCGA 574
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 AlaSerArgTrpProArgSerAlaSerArgTrpProTrpSerAlaGlyLeuThrValArg
                                                                                                                                                                                                                                                                                                                                              GATCGTCCGCAACTGGGGCGAGCTGTGCATGGGGCGTGGC 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 AspArgProGlnLeuGlyGluLeuCysMetGlyArgGly 79
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Matches:
Conservative:
Mismatches:
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|mol_type="mkna"
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clone_lib="UI-CF-FN0"
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/tissue_type="Gatedarthritic Cartilage"
/dav stage="Adult"
/lab_host="Hilds (Life Technologies)"
/clone lib="NGI Cacor Technologies)"
/clone lib="NGI Cacor Technologies"
/clone lib="NGI CAPP Ct1"
/note="Grgan: Knee; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR 1: Site 2: Not 1:
NGI CGAP Ct1 is a normalized CDNA library containing the following tissue(s): Osteoarthritic Cartilage The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was prined with an oligo-dT primer containing a Not I site. Double stranded CDNA was ligated to an EcoR I
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
POLYA=Yes.
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a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was subtracted according to Bonaldo, Lennon and Soares, Genom Research, 6:791-806, 1996. The tissue was provided by Dr. TAG TISSUE-Human Lung Aveolar Macrophage TAG LIB-UI-H-FTAT TAG-LIB-UI-H-TAG TAG-LIB-UI-H-TAG TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG-LIB-UI-H-TAG
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|db_xref="taxon:9606"
|clone="UI-H-EUI-bac-p-06-0-UI"
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/organism="Homo sapiens"
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Tel: +55-11-2704922
Fax: +55-11-2707001
Email: saimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtmi2.pl?tl=PMI&t2=PMI-NN1084-240900-005-962&t2=2000-09-24&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 27
High quality sequence start: 27
High quality sequence stop: 282.
Location/Qualifiers
1. .28

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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Meteria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 282)
Dias Neto,B., Garcia Correa,R., Verjovski-Almeida,S., Eriones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Brunstein,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF364571

282 bp mRNA linear EST 24-NOV-2000
PMI-NNI084-240900-005-g05 NNI084 Homo sapiens cDNA, mRNA sequence.
BF364571
BF364571.1 GI:11326596
                                                                                                                                                                                                                       10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Homo sapiens (human)

Homo sapiens

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AGENCOURT 6553891 NIH_MGC_71 Homo sapiens cDNA clone IMACE:5555626
5', mRNA sequence.
BM806108
adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is TAG_TISSUE-osteoarthritic cartilage TAG_LIB-UI-H-BUI
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/db_xref="ptaxon:0986" "
/lab_host="E. coli DH128"
/lab_host="E. coli DH128"
/clone="ptaxon:0980" |
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/clone="btaxon:0980" |
/clon
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(bases 1 to 163)
Sakai, D., Tong, H.-S. and Minkin, C.
Osteoclast Molecular Phenotyping by Random cDNA Sequencing
Bone 17 (2), 111-119 (1995)
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University of Southern California
USC School of Dentistry, 925 West 34th Street, DEN-4220, Los
Angeles, CA 90089-0641
Tel: 2137405563
Eax: 2137407560
Email: sakai@molbio.usc.edu
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/mol_type="mRNA"
/strain="New Zealand White"
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Oryctolagus cuniculus
                                                                                                                     US-09-972-032-2 (1-79) x BF364571 (1-282)
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Location/Qualifiers
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21.52%
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R86559.1 GI:947213
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AUTHORS
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JOURNAL
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PUBMED
COMMENT
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79 rcacecreeccaaearceecaaeccec 105

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AA656691 LEST 04-NOV-1997 WENA linear EST 04-NOV-1997 vp95c01.rl Stratagene mouse diaphragm (#937303) Mus musculus cDNA clone IMAGE:1092480 5', mRNA sequence.
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                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 181)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., The Leising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
MGI:598712
Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 163.
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                       Unpublished (1996)
Contact: Marra M/Mouse EST Project
Washington University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
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The WashU-HHMI Mouse EST Project
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                                                                                                                 Mus musculus (house mouse)
Mus musculus
                                                               AA656691
AA656691.1 GI:2592845
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EST.
Homo sapiens (human)
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KEYWORDS
SOURCE
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Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryotta; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

The (SAP http://www.ncbi.nlm.nih.gov/ncicgap.
Notional Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

Tumor Gene Index

Tumor Gene Index

The Contact: Robert Straubberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert--Buck, M.D., Ph.D.

CDNA Library Preparation: Stratagene, Inc.

CDNA Library Preparation: Stratagene, Inc.

CDNA Library Arrayed by: Gap Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NOI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LiNL at:

Seq primer: -40m13 fwd ET from Amersham

High quality Sequence stop: 1

1.4240 (Qualifiers)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
TITLE
                                                                                                                                               JOURNAL
COMMENT
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Homo sapiens

ORGANISM

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 100.00% 100.00% 11.39% Percent Similarity: Best Local Similarity: Query Match: Alignment Scores: Pred. No.:

US-09-972-032-2 (1-79) x AA593543 (1-424)

374 TGGACAGGCTCGGAGAAGGCCAGGAG 400 23 TrpThrGlyLeuGlyGluGlyGlnGlu 31 δ

Search completed: July 13, 2004, 15:53:46 Job time : 2893 secs

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Title: Perfect score:

Sequence:

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OM protein

Run on:

Scoring table:

Minimum DB Maximum DB

Searched

Database

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44624, A
1393, Ap
34802, A
13, Appl
1, Appli
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; Sequence 1, Application US/09972032
; Publication No. US20020086361A1
; GENERAL INFORMATION:
; APPLICANT: Case Western Reserve University
; APPLICANT: Sutton, Amelia
; TITLE OF INVENTION: A Modulator of Antiestrogen Pharmacology
FITE OF INVENTION: A Modulator of Antiestrogen Pharmacology
FITE OF INVENTION: A Modulator of Antiestrogen Pharmacology
FILE REFERENCE: 27708/04003
; CURRENT APPLICATION NUMBER: US/09/972,032
; CURRENT PILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 60/238,190
PRIOR PILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
: LENGTH: 990
US-09-972-032-1
US-10-369-793-44624
US-10-299-793-44624
US-10-299-793-44624
US-10-132-134-13
US-10-132-134-13
US-10-132-134-13
US-10-245-13111
US-10-245-103-111
US-10-245-103-111
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US-10-23-23-23-111
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US-09-972-032-1
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-MODEL=frame+ p2n.model - DEV=xlh
-MODEL=frame+ p2n.model - DEV=xlh
-MODEL=frame+ p2n.model - DEV=xlh
-DE-PUDIIshed Applications NA -QFWN=fastap - SUFFIX=rnpb - MINNATCH=0.1
-DB=PUDIIshed Applications NA -QFWN=fastap - SUFFIX=rnpb - MINNATCH=0.1
-LOOPCIL=0 - LOOPERXT=0 - UNITS=bits - START=1 - MARTAIX=blosum62
-TRANS=human40.cdi _LIST=45 - DOCALIGN=200 - THR _SCORE=pct - THR _MAX=100
-THR _MIN=0 - ALIGN=15 - MODE=LOCAL - OUTFWT=pto - NORM=ext - HEAPBJIZE=500 - MINLEN=0
-MAXIEN=200000000 - USER=US09972032 @CGN 1 1 511 @runat - 06072004 121455_8495
-NCPUS=6 - ICPUS=3 - NO MMAP - LARGEQUERY - NEG $CORES=0 - WAIT - DSPBLOCX=100
-LONGLOG - DEV TINEOUT=120 - WARN TIMEOUT=30 - THREADS=1 - XGAPOP=10 - XGAPEXT=0.5
-FGAPOP=6 - FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
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                                                                                                               (without alignments)
955.426 Million cell updates/sec
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1. /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2. /cgn2_6/ptodata/2/pubpna/USO6_NEW PUB.seq:*
3. /cgn2_6/ptodata/2/pubpna/USO6_NEW PUB.seq:*
4. /cgn2_6/ptodata/2/pubpna/USO6_NEW PUB.seq:*
5. /cgn2_6/ptodata/2/pubpna/USO6_NEW PUB.seq:*
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7. /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
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11: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
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19: /cgn2_6/ptodata/2/pubpna/USO0_NEW PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/USO0_NEW PUB.seq:*
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1 MCGRPRRVSAGCGFADAHWT.....SAGLTVRDRPQLGELCMGRG
                                                                                             July 12, 2004, 18:17:11 ; Search time 403 Seconds
      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                  nucleic search, using frame plus p2n model
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Ygapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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seg length: 200000000
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Score

Result Š.

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us-09-972-032-2_1.rnpb

Db	RESULT 3 US-10-292-798-1393/c ; Sequence 1393, Application US/10292798 ; Publication No. US20030235833A1 ; APPLICANT: SUWA, MAXIKO	; APPLICANT: ASAI, KIYOSHI ; APPLICANT: AKIYAMA, YUTAKA ; APPLICANT: ARIXAMI, HIROYUKI ; APPLICANT: ABURATANI, HIROYUKI ; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS	; FILE REFRENCE: 084335/166 ; CURRENT APPLICATION NUMBER: US/10/292,798 ; CURRENT FILING DATE: 2002-11-13 ; PRIOR APPLICATION NUMBER: 10/017,161	; PRICR FILING DATE: 2001-12-18 ; PRIOR SPLICATION NUMBER: UP 2001-246789 ; PRIOR FILING DATE: 2001-06-18 ; NUMBER OF SEQ ID NOS: 2070	; SOFTWARE: Patentin Ver. 2.1 ; SEQ ID NO 1393 ; LENGTH: 822900 ; TYPE: DNA ; ORCANISM: Homo sapiens	FEATURE: J. COCATION: Source FRATIDE:	••			; NAME/KEY: CDS ; LOCATUN: (261786)(261845) ; FEATURE:	; NAME/KEY: CDS ; CONTION: (273663)(273702)	; FAMIUKEY: CDS ; LOCATION: (347633)(347711)	; FEATURE: ; NAME/KRY: CDS ; LOCATION: (482589)(482596)		; NAME/KEY: CDS ; LOCATION: (822485)(822700) ; FEATURE:	NAMES/KEY: modified base; LOCATION: (4848)[4947); OTHER INFORMATION: a, t, c, g, unknown or other	36 }	; OTHER INFORMATION: a, t, c, g, unknown or other ; FRATURE:	; NAME/KEY: modified_base ; LOCATION: (17785)(17884) ; OTHER INFORMATION: a, t, c, g, unknown or other	; FEATURE: ; NAME/KEY: modified_base ; LOCATION: (61159)(61258) ; OTHER INFORMATION: a, t, c, g, unknown or other
Pred. No.: 1.22e-36 Length: 990 Score: 456.00 Matches: 79 Percent Similarity: 100.00\$ Conservative: 0 Best Local Similarity: 100.00\$ Mismatches: 0 Query Match: 13 Games 14 Ga	D9-972-032-2 (1-79) x US-09-972-032-1 (1-990) MetCysGlyArgProArgArgValSerAlaGlyCysGly	OY 21 GlyLeuTrpThrGlyCluGlyGluGlyGluGlyGlyCluGlyGlyBroGluGlyGlnAla 40	Oy 41 SerProThrProAspCysAlaSerArgTrpProArgSerAlaSerArgTrpProTrpSer 60	Oy 61 AlaGlyLeuThrValArgAspArgProglnLeuGlyGluLeuCysMetGlyArgGly 79 bb 383 GCAGGTCTTACGTCCGAGATCGTCGCAACTGGGCGAGCTGTGCATGGGGCGTGGC 439	RESULT 2 US-10-369-493-44624 ; Sequence 44624, Application US/10369493 ; Publication No. US20030233675A1	; GENERAL INPORMATION: ; APPLICANT: Cao, Yongwei ; APPLICANT: Hinkle, Gregory J.	; APPLICANT: Slater, Steven C.; APPLICANT: Slater, Steven C.; APPLICANT: Goldman, Barry S.	; AFFLICANT: Chen, Xiableng ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES ; FILE REPERENCE: 38-10 (52052) B	CURRENT APPLICATION NUMBER: 18/10/369,493 CURRENT APPLICATION NUMBER: 2003-02-28 DRIOD ADDITIONAL MINGRED: 10 6/1260 030	FALOR FILLING DATE: NORTHER: US 80/380,039 FALOR FILLING DATE: 2002-02-21 JUMBER OF SEQ ID NOS: 47374	; SEQ ID NO 44624 ; LENGTH: 3642 ; TYPE: DNA	; ORGANISM: SYNECHOCOCCUS SP. WH 8102 US-10-369-493-44624	2.92 Length: 95.00 Marches:	ercent Similarity: 39.56\$ Conservative: est Local Similarity: 34.07\$ Mismatches: 20.83\$ Indels:	L6 09-972-032-2 (1-79) x US-10-369-493-44624 (1-3642)	CysGlyPheAlaAspAlaHisTrpThr	21	Db 2880 GGAIGCGTICCCGCAGCTGGACCIGGTGAACCAGGCACAACAGATGGTGGCCTTGCT 2939	Qy 33GlylleGlyProGluGlyGlnAlaSerProThrProAspCys 46	7 T

us-09-972-032-2 1.rnpb

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FEATURE KEY: modified base
LOCATION: (370285)...(370287)
OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified base
LOCATION: (370289)...(370291)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (409961)..(410060)
OTHER INFORMATION: a, t, c, g, unknown or other
FOATURE:
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LOCATION: (385643) ... (385742)
OTHER INFORMATION: a, t, c, g, unknown or other
KEY: modified base
ION: (67605)..(67704)
INFORWATION: a, t, c, g, unknown or other
                                                                                                                                                                                                             FORTHWEY KEY: modified base
LOCATION: (85854). (85953)
OTHER INFORMATION: a, t, c, g, unknown or other
                                                                                                                                                                                                                                                                                                                        NAME/KEY: modified base
LOCATION: (367573) ... (367573)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (367588)...(367588)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (367595)..(367595)
OTHER INFORMATION: a, t, c, g, unknown or other
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THER INFORMATION: a, t, c, g, unknown or other
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CCCATION: (367985)...(367985)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (367993)...(367993)
DTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (367995)..(367996)
PTHER INFORMATION: a, t, c, g, unknown or other
PATHURE:
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DECALION: (367998)...(367998)
THER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (370273)..(370277)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (370279) ... (370279)
DIHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (370281) ... (370282)
DTHER INFORMATION: a, t, c, g, unknown or other
                                                                                                     NAME/KEY: modified base
LOCATION: (74625)...(74724)
OTHER INFORMATION: a, t, c, g, unknown or
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822900 Length:
Matches:
Conservative:
Mismatches: NAME/KEY: modified base LOCATION: (410096)...(410096) OTHER INFORMATION: a, t, c, g, unknown or other FEMTURE:
NOAMINGET: modified base
NOAMINGT: (727470)..(727569)
OTHER INFORMATION: a, t, c, g, unknown or other NAME, KEY: modified base LOCATION: (730296)...(730395) OTHER INFORMATION: a, t, c, g, unknown or other NAME/KEY: modified base LOCATION: (731863) ... (731962) OTHER INFORMATION: a, t, c, g, unknown or other NAME, KEY: modified base LOCATION: (735752)...(735851) OTHER INFORMATION: a, t, c, g, unknown or other NAME/KEY: modified base LOCATION: (738576). (738675) OTHER INFORMATION: a, t, c, g, unknown or other NAME/KEY: modified base LOCATION: (740924)...(741023) OTHER INFORMATION: a, t, c, g, unknown or other LOCATION: (748430) ... (748529)
OTHER INFORMATION: a, t, c, g, unknown or other FEATURE:
NAME/KEX: modified base
NAME/KEX: modified base
OTHER INFORMATION: a, t, c, g, unknown or other NAME/KEY: modified base LOCATION: (728849) ... (728948) OTHER INFORMATION: a, t, c, g, unknown or other NAME/KEY: modified base LOCATION: (734124)...(734223) OTHER INFORMATION: a, t, c, g, unknown or other NAME/KEY: modified base LOCATION: (734441) ...(734441) OTHER INFORMATION: a, t, c, g, unknown or other NAME/KEY: modified base LOCATION: (744350)...(744459) OTHER INFORMATION: a, t, c, g, unknown or other NAWE/KEY: modified base LOCATION: (726106)...(726205) OTHER INFORMATION: a, t, c, g, unknown or other or other unknown FEATURE:
NAME/KEY: modified base
LOCATION: (724960)..(725059)
OTHER INFORMATION: a, t, c, g, FEATURE: NAME/KEY: modified_base LOCATION: (754323)..(754422) 348 95.00 37.39% 32.17% 20.83% NAME/KEY: modified_base Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: FEATURE: NAME/KEY: EATURE:

US-09-972-032-2 (1-79) x US-10-292-798-1393 (1-822900)

Qy 45 AspCysAlaSerArgTrpProArgSerAlaSerArgTrpProTrpSerAla 61	RESULT 5 US-10-132-134-13 Sequence 13, Application US/10132134 Sequence 13, Application US/10132134 Sequence 13, Application No. US20030171562A1 September 1 NFORMATION: APPLICANT: Farnet, Chris APPLICANT: Staffa, Alfredo APPLICANT: Staffa, Alfredo APPLICANT: Staffa, Alfredo APPLICANT: Assopoulos, Emmanuel TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES FILE REFERENCE: 3012-2US CURRENT APPLICATION NUMBER: US/10/132,134 CURRENT APPLICATION NUMBER: US/10/132,134 NUMBER OF SEQ 1D NOS: 43 SOFTWARE: Patentin version 3.0	TYPE: DNA 13 15 17 17 17 17 17 17 17	08-09-972-032-2 (1-79) x US-10-132-134-13 (1-24081) QY 9 SerAlaGlyCysGlyPheAlaAspAlaHisTrpThrGlyLeuTrpThrGlyLeuGly-Gl 28	Qy 61 aGlyLeuThrValArg 66 Db 12670 CTCCTGGCCGCCCGC 12685 RESULT 6 US-10-132-134-1 ; Sequence 1, Application US/10132134 ; Publication No US20030171562A1 ; GENERAL INPORMATION:	APPLICANT: Farnet, Chris APPLICANT: Yang, Xianshu APPLICANT: Sazépoulos, Emmanuel TILLS OF INVENTION: POLYKETIDE SYNTHASE ENZYMES TILLS OF INVENTION: POLYKETIDE SYNTHASE ENZYMES CURRENT APPLICATION NUMBER: US/10/132,134 CURRENT APPLICATION NUMBER: US/10/132,134 CURRENT APPLICATION NUMBER: US/10/132,134 CURRENT APPLICATION NUMBER: US/10/132,134 CURRENT PILING DATE: 2002-04-26 NUMBER OF SEQ ID NOS: 43 SOFTWARE: Patentin version 3.0 SEQ ID NO 1 LENGTH: 52101 TYPE: DNA
Qy 3 GlyArgProArgArgValSerAlaGlyCysGlyPheAlaAspAlaHisTrpThrGlyLeu 22	Qy 32		TITLE OF INVENTION: RICE NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH CONTINUING PLANTS and USES Thereof for Plant Improvement; PILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 34602 LENGTH: 6395 TYPE: DAA CRANTSM: Oryza sativa PEATURE: COTHER INFORMATION: Clone ID: PAT_MRT4530_38782C.1	Alignment Scores: Pred. No.: Percent Similarity: Pred. S.	QY 5 ProArgArgValSerAlaGlyCysGlyPheAlaAspAlaHisTrpThrGlyLeu 22 Db 5977 CCTTCTGCTGCAGGGGATTCTGCTGTTCAGAAGATGCACCAGCTTGGACTGGGTTA 5918 QY 23

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               CysGlyArgProArgArgValSer---AlaGlyCysGlyPheAlaAspAlaHisTrpThr 20
                                                                                                                 --LeuglyGluGlyGlnGluGlyGlyIleGlyProGlu 37
                                                                                                                                                                                                                                                                                                                    38 GlyGlnAlaSerProThrProAspCysAlaSerArgTrpProArgSerAlaSerArgTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ION: ACIDS ENCODING THE SAME
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CURRENT APPLICATION NUMBER: US/10/245,752
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Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
Watambe, Colin
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, Sequence 111, Application US/10245752
; Publication No. US20030064473A1
, GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                        72 GlyGluLeuCysMetGly 77
                                                                                                                    21 GlyLeuTrpThrGly--
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Fong, Sherman
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; ORGANISM: Homo Sapien
US-10-245-752-111
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Pred. No.:
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GENERAL INVENTATION,
GENERAL INVENTATION,
APPLICANT: Labas, Valid, A.
APPLICANT: Labas, Valid, A.
APPLICANT: Labas, Valid, A.
APPLICANT: Action of the control of the
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                                                                                                                                                                                                                                                                                                                         9 SerAlaGlyCysGlyPheAlaAspAlaHisTrpThrGlyLeuTrpThrGlyLeuGly-Gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 r------ArgTrpProArgSer----AlaSerArgTrpPro---TrpSerAl
                                                                                                                                                                                                                                                                                                                                                                                                                           28 uGlyGlnGluGlyGlyIleGlyProGluGlyGlnAlaSerProThrProAspCysAlaSe
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81
18
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Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
, ORGANISM: Streptomyces platensis subsp. rosaceus US-10-132-134-1
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Matches:
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                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
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252 ACGCACATGACTGTGAGGCGCTGGGGCTCCGAGGCAGCCGGCTTCCAGGGGTCCC 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        432 CCGACGCCCCGTGCTGGGAGGAGGCCATGGCCGCTGCATTCCAACTGGCGAGTTTTGTCC 491
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CURRENT APPLICATION NUMBER: 105/10/245,103
CURRENT FILING DATE: 2002-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 CysGlyArgProArgArgValSerAlaGlyCysGlyPheAlaAspAlaHisTrpThrGly
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PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 111
LENGTH: 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 LeuTrpThrGlyLeuGlyGluGlyGluGluGlyGlyIleGlyProGlu-
                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
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Filvaroff, Ellen
Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
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29.51%
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                              TYPE: DNA
CRGANISM: Homo
US-10-245-859-111
                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
Pred. No.:
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US-10-245-103-111
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APPLICANT: WATCOTIA
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APPLICANT: PROOF, SHETTIAM
APPLICANT: PROOF, SHETTIAM
APPLICANT: PRIOR SECRETED AND TRANSMEBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R1C8
FILE REFERENCE: P3630R1C8
FILE REFERENCE: P3630R1C8
FILE REPERENCE: P3630R1C8
FILE REPERENCE: P3630R1C9
FRICK APPLICATION NUMBER: 10/19942
FRIOR FILING DATE: 1997-10-10
FRIOR APPLICATION NUMBER: 60/065027
FRIOR FILING DATE: 1998-11-10
FRIOR FILING DATE: 1998-13-27
FRIOR FILING DATE: 1998-13-27
FRIOR FILING DATE: 1998-06-02
FRIOR APPLICATION NUMBER: 60/09699
FRIOR FILING DATE: 1998-06-02
FRIOR FILING DATE: 1998-06-02
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     36
7
134
848
6
                            Conservative:
Mismatches:
Indels:
                                                                                                                                                              x US-10-245-752-111 (1-943)
     Matches:
                                                                                                           Gaps:
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Grimald, J. Christopher
Gurney, Austin
Smith, Victoria
Srephan, Jean Phillippe
Watanbe, Colin
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Publication No. US20030064474A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
93.50
35.25%
29.51%
20.50%
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                            Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                           US-09-972-032-2 (1-79)
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US-10-245-859-111
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APPLICANT: Stephan, Jean, Phillippe
APPLICANT: Wood, William
APPLICANT: Tatanbe, Colin
APPLICANT: Pong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT FILING DATE: 2002-09-16
PRIOR FILING DATE: 1097-00-18
PRIOR PELICATION NUMBER: 60/053014
PRIOR FILING DATE: 1997-10-24
PRIOR PELICATION NUMBER: 60/053016
PRIOR FILING DATE: 1997-10-24
PRIOR PELICATION NUMBER: 60/05301
PRIOR FILING DATE: 1998-05-22
PRIOR PELICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-02
PRIOR PELICATION NUMBER: 60/089801
PRIOR PELING DATE: 1998-06-24
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                                         Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
Wood, William
Zhang, Zemin
Fong, Sherman
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ORGANISM: Homo Sapien
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Best Local Similarity:
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Pred. No.:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-10-24
PRIOR PLING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/06507
PRIOR FILING DATE: 1997-11-10
PRIOR PILING DATE: 1997-11-10
PRIOR PILING DATE: 1998-03-27
PRIOR PILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR PILING DATE: 1998-06-22
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-25
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; Sequence 111, Application US/10245107
; Publication No. US20030068779A1
; GENERAL INFORMATION:
; APPLICANT: Baker; Kevin
; APPLICANT: Eaton, Dan
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93.55
35.25
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COGANISM: Homo Sapien
US-10-245-103-111
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Goddard, Audrey
Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
Wood, William
Zhang, Zemin
Fong, Sherman
Fong, Sherman
Fong, Sherman
Fong, Sherman
Fong, Sherman
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Publication No. US20030068781A1
GENERAL INFORMATION:
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Filvaroff, Ellen
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; ORGANISM: Homo Sapien
US-10-245-771-111
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LENGTH: 943
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APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
APPLICANT: Pong, Sharman
TILLE OF INVENTION: BCIDE BNCODING THE SAME
FILER REFERENCE: P3630R1C90
CURRENT APPLICATION NUMBER: US/10/245,143
CURRENT APPLICATION NUMBER: US/197942
PRIOR FILING DATE: 2002-07-18
PRIOR FILING DATE: 2002-07-18
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-05-22
PRIOR FILING DATE: 1998-05-22
PRIOR FILING DATE: 1998-06-08
PRIOR FILING DATE: 1998-06-08
PRIOR FILING DATE: 1998-06-08
PRIOR FILING DATE: 1998-06-08
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-25
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                                                                                                                                                                                                     Sequence 111, Application US/10245143
Publication No. US20030068780A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            Goddard Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
Wood, William
66 gAspArgProGlnLeu--
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APPLICANT: Baton, Dan
APPLICANT: Filvaroff, El.
APPLICANT: Goddard, Audri
APPLICANT: Grimaldi, J. (APPLICANT: Grimaldi, J. (APPLICANT: Gurney, Austin
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ORGANISM: Homo Sapien
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Best Local Similarity:
Query Match:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE OF INVENTION: ACIDS ENCODING THE SAME FILE OF INVENTION: ACIDS ENCODING THE SAME FILE SERRENCE: PASSORACIOS CURRENT APPLICATION NUMBER: US/10/245,771

CURRENT PILING DATE: 2002-09-16

PRIOR PELING DATE: 2002-07-18

PRIOR FILING DATE: 1997-09-17

PRIOR PELING DATE: 1997-09-17

PRIOR PELING DATE: 1997-10-24

PRIOR PELING DATE: 1997-11-10

PRIOR PELING DATE: 1997-11-10

PRIOR PELING DATE: 1998-05-22

PRIOR PELING DATE: 1998-06-22

PRIOR PELING DATE: 1998-06-18

PRIOR PELING DATE: 1998-06-18

PRIOR PELING DATE: 1998-06-18

PRIOR PELING DATE: 1998-06-24

52 ACGCACATGACTGTGAGGCGCTGGGGCTCCGAGGCAGCCGGCTTCCAGGAGTCCC 311
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                                                                                                                                               -GlyGlnAlaSerProThrPro 44
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                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-245-851-111
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Best Local Similarity:
Query Match:
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APPLICANT: Baker, Kevin
APPLICANT: Baker, Kevin
APPLICANT: Baker, Kevin
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Applicanton Women: 10/197942
TITLE OF INVENTION: SECRETED AND THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-11-10
PRIOR PILLING DATE: 1997-11-10
PRIOR PILLING DATE: 1999-11-10
PRIOR PILLING DATE: 1999-11-10
PRIOR PILLING DATE: 1999-11-10
PRIOR PILLING DATE: 1999-05-22
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312 GAGGCACCGTCAAACTGCAGTTCGACATGATGCGCGCCTGCAACCTGGTGGCCACGGCCG 371
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36
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                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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Publication No. US20030068782A1
GENERAL INFORMATION:
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                 1.25
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252 ACGCACATGACTGTGAGGCGCTGGGGCTCCGAGGCAGCCGGCTTCCAGGAGTCCC 311
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312 GAGGCACCGTCAAACTGCAGTTCGACATGATGCGCGCCTGCAACCTGGTGGCCCACGGCCG 371
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PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR FLIING DATE: 1998-06-18
PRIOR PLIING DATE: 1998-06-24
PRIOR PLIING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 111
LENGTH: 943
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Matches:
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APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watanbe, Colin
APPLICANT: Wood, William
APPLICANT: Pang, Zamin
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; Sequence 111, Application US/10245883
; Publication No. US20030068783A1
; GENERAL INFORMATION:
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198 TGGTGGACCCGGGGGGGGCCGA----GCCCTGGGGCCAGAGCCGGCCAGGTGG 251
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CURRENT APPLICATION NUMBER: US/10/245,883

CURRENT FILING DATE: 2002-09-16

PRIOR APPLICATION NUMBER: 10/197942

PRIOR APPLICATION NUMBER: 10/197942

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-10-24

PRIOR FILING DATE: 1997-10-24

PRIOR FILING DATE: 1997-10-24

PRIOR FILING DATE: 1997-10-24

PRIOR PELING DATE: 1998-01-27

PRIOR PELING DATE: 1998-01-27

PRIOR PELING DATE: 1998-05-27

PRIOR FILING DATE: 1998-05-22

PRIOR PLING DATE: 1998-05-22

PRIOR PLING DATE: 1998-05-22

PRIOR PLING DATE: 1998-06-34

PRIOR FILING DATE: 1998-06-35

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; ORGANISM: Homo Sapien
US-10-245-883-111
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Search completed: July 12, 2004, 19:34:50 Job time : 586 secs us-09-972-032-2 1.rni

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July 10, 2004, 16:42:00 ; Search time 71 Seconds (without alignments) 617.481 Million cell updates/sec
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456
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 1008
Listing first 45 summaries
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Ygapop 10.0 , Ygapext (
Fgapop 6.0 , Fgapext (
Delop 6.0 , Delext :
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                          Title:
Perfect score:
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                                                                                                                                                                                                                                Sequence:
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Issued_Patents_NA:*
1: /cgfl2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 5885, Ap	Sequence 171, App	Sequence 1, Appli	Sequence 1180, Ap		Sequence 5342, Ap	Sequence 5304, Ap	Sequence 5231, Ap	Sequence 5260, Ap	Sequence 2, Appli	Sequence 1, Appli	Sequence 1, Appli
	ID	US-09-252-991A-5885	US-09-614-912-171	US-09-433-248A-1	US-09-023-655-1180	US-09-621-976-12967	US-09-252-991A-5342	US-09-252-991A-5304	US-09-252-991A-5231	US-09-252-991A-5260	US-09-103-840A-2	US-09-103-840A-1	US-09-773-816-1
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	Query Match Length DB	558	2043	1386	3625	497	603	606	981	2592	4403765	19.0 4411529	23673
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	Score	93	16	88	88	87.5	86.5	86.5	86.5	86.5	86.5	86.5	98
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-08-753-247-1	8-753-247-1	-08-753-247	-08-753-247	-08-753.	-08-477-254A-	å	08-428	-713-556	08-75	-07-885-972	08-745-88	-480-	-10-133-91	-07-885-972	08-745-	-08-480-3	-09-841-	-09-252-991A-13	-09-252-991A-92	-09-252-991A-9	-252-991A-92	-09-252-991A-13	-09-252-991A-79	-09-252-991A-82	-09-252-991A-	09-105-	-09-614-912-1	09-252-991A-8	-09 - 851 - 8	-850-9	-08-125-468	US-08-474-933-1
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ALIGNMENTS

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-60-SD	US-09-252-991A-5885			
; Sedu	Sequence 5885, Application US/09252991A	ation US/09252	991A	
; Pate	Patent No. 6551795			
; GENE	GENERAL INFORMATION:			
; APP	LICANT: Marc J.	Rubenfield et	а1.	APPLICANT: Marc J. Rubenfield et al.
; TIT	LE OF INVENTION:	NUCLEIC ACID	AND AMINO ACID S	EQUENCES RELATING TO PSEUDOMONAS
TIL '	TITLE OF INVENTION:	AERUGINOSA FC	AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS	D THERAPEUTICS
; FIL	FILE REFERENCE: 107196.136	7196.136		
CUR!	CURRENT APPLICATION NUMBER: US/09/252,991A	NUMBER: US/09/	252,991A	
, CURI	CURRENT FILING DATE: 1999-02-18	1999-02-18		
; PRI	PRIOR APPLICATION NUMBER: US 60/074,788	MBER: US 60/0	74,788	
; PRI	PRIOR FILING DATE: 1998-02-18	1998-02-18		
, PRI	PRIOR APPLICATION NUMBER: US 60/094,190	MBER: US 60/0	94,190	
PRI	PRIOR FILING DATE: 1998-07-27	1998-07-27		
MUM.	NUMBER OF SEC ID NOS: 33142	3: 33142		
SEO	SEQ ID NO 5885			
E .	LENGIH: 558			
, TY	TYPE: DNA			
, ORC	ORGANISM: Pseudomonas aeruginosa	las aeruginosa		
60-SD	US-09-252-991A-5885			
Alignm	Alignment Scores:			
Pred. No.:	No.:	2.52	Length:	558
Score:		93.00	Matches:	28
Percen	Percent Similarity:	38.30%	Conservative:	8
Best L	Best Local Similarity:	29.79%	Mismatches:	26
Query Match:	Match:	20.39%	Indels:	32
DB:		4	Gaps:	4,
-60-SD	US-09-972-032-2 (1-79) x US-09-252-991A-5885 (1-558)	x US-09-252-99	1A-5885 (1-558)	
λŏ	4 ArgProArg	JArgValSerAlaGl	yCysGlyPheAlaAsp	ArgProArgArgValSerAlaGlyCysGlyPheAlaAspAlaHisTrpThrGlyLeuTrp 23
d d	207 CGTCCTCG	ACGTGCCGCCGCAGG	ATGTGATTTCCCGCGA	CGTCCTCGACGTGCCGCGCAGGATGTGATTTCCCGCGACAACGTTTC 254

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415 cerrasacrecesacariscesesesacesissecresesacioner---rassantesa-- 361
   22 LeuTrpThrGlyLeuGlyGluGlyGluGlyGlyJleGlyProGluGlyGlnAlaSer 41
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                                                                                                                                Pro---ThrProAspCysAlaSerArgTrpProArgSerAlaSerArgTrpProTrpSer
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US-09-023-655-1180/Application US/09023655
Factor No. 6607879
Fatent                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----GlyGlnGluGlyGlyIle
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Conservative:
Mismatches:
Indels:
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APPLICANT: Fancou, Omolayo O.
APPLICANT: Famodu, Omolayo O.
APPLICANT: Han, Feng
APPLICANT: Rafalski, J. Antoni
ITLE OF INVENTION: Disease Resistance Factors
FILE BEFERANCE: BB1252 US NA
CURRENT APPLICATION NUMBER: US/09/433,248A
CURRENT APPLICATION NUMBER: 1999-11-04
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
                                                                                                                                                                                                                                                                                                                         360 GAAGGACTCGAAATCAGACACGAACCCATACTT 328
                                                                                                                                                                                                                                                            61 AlaGlyLeuThrValArgAspArgProGlnLeu 71
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; Sequence 1, Application US/09433248A
; Patent No. 6355462
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SOFTWARE: Microsoft Office 97
SEQ ID NO 1386
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Best Local Similarity:
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Pred. No.:
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                                     255 ------GGTGAAGGTCAACGGGTGGTGTACTTCCGCGTGCTCGATCCGCAGGAAGG 305
                                                                                                                                                                                      536
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                                                                                                                                                                                                                                                            .-----SerAlaSerArgTrpPro 58
ThrGlyLeuGlyGluGlyGlnGluGlyGlyIleGlyProGluGlyGlnAlaSer---- 41
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APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Grozeo, Buddy
APPLICANT: Famedu, Gou-Hau
APPLICANT: Famedu, Goulayo O.
APPLICANT: Famedu, Goulayo O.
APPLICANT: Sakai, Hajime
APPLICANT: Grami, Perry G
APPLICANT: Grami, Perry G
APPLICANT: Anderson, Shawn
TITLE OF INVENTION: Plant Metabolism Genes
FIER REFERENCE: BB1378 US NA
CURRENT APPLICATION NUMBER: US/09/614,912
CURRENT APPLICATION NUMBER: G0/143,401
FRIOR APPLICATION NUMBER: G0/143,401
FRIOR FILING DATE: 1999-07-12
FRIOR FILING DATE: 1999-07-12
FRIOR APPLICATION NUMBER: G0/143,401
FRIOR FILING DATE: 1999-12-12
FRIOR APPLICATION NUMBER: G0/143,401
FRIOR APPLICATION NUMBER: G0/143,401
FRIOR PILING DATE: 1999-12-15
FRIOR APPLICATION NUMBER: G0/172,959
FRIOR FILING DATE: 1999-12-21
FRIOR APPLICATION NUMBER: G0/172,946
FRIOR FILING DATE: 1999-12-21
                                                                                                                                                                                                                                                         --SerArgTrpProArg-
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; Sequence 171, Application US/09614912
; Patent No. 6677502
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
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LENGTH: 2043
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RESULT 6

US-09-252-991A-5342/C

Sequence 5342, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES

CURRENT APPLICATION NUMBER: US 60/094,190

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-07-27

WUMBER OF SEQ ID NOS: 33142

LENGTH: 603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 TrpThrGlyLeuTrpThrGlyLeuGlyGluGlyGlnGluGlyGlyIleGlyProGluGly 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 GlnAlaSerProThrPro------AspCysAlaSerArgTrp-Pro---
                                                                                                                                                                                                                                                                                                                                                                                    497
21
4
115
115
3
                APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 0549R2
CURRENT APPLICATION WUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
LENGTH: 497
LENGTH: 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-972-032-2 (1-79) x US-09-621-976-12967 (1-497)
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ADDRESSEE: INCYTE PHARTMACOLLE...
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UGA
ZIP: 94304
COMPUTER: LEOPON:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS GOERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS GOERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS GOERATING DATE: HEREWITH
CLASSIFICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION NUMBER:
FILING DATE: CLASSIFICATION:
APPLICATION NUMBER: 37,071
REFERENCE/DOCKET NUM
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US-09-621-976-12967/C
; Sequence 12967, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
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35.96%
19.30%
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Best Local Similarity:
Query Match:
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US-09-023-655-1180
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Pred. No.:
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Sequence 5260, Application US/09252991A
Sequence 5260, Application US/09252991A
Sequence 5260, Application US/09252991A
Sequence 5260, Application
GENERAL INFORMATION:
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION WUMBER: US 60/074,788
PRIOR APPLICATION WUMBER: US 60/074,788
PRIOR PLILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR PLILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33.442
SEQ ID NOS: 33.442
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                                                981
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APPLICANT: FLEISCHMAN, ROBERT D. APPLICANT: WHITE, Owen R.
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                                                18.1
86.50
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Best Local Similarity:
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Best Local Similarity:
Query Match:
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US-09-252-991A-5260
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             Alignment Scores:
Pred. No.:
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US-09-103-840A-2
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US-09-252-991A-5304/c

Squence 5304, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICATION:

APPLICATION WULLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 5304

LENGTH: 309

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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 5211
LENGTH: 981
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::: ||||||| ::: ||||||| 114 ATCGCCAACGCCCGAAAGCAGCCCCTGTT---CGAGCAGGC
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Matches:
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Mismatches:
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CRGANISM: Pseudomonas aeruginosa
US-09-252-991A-5231
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Best Local Similarity:
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US-09-252-991A-5231
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US-09-252-991A-5304
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                                                                                                                                                                                                                                                                                                                                                                                                 59
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                                                                                                                                                                       CysGlyArgProArgArgValSerAlaGlyCysGlyPheAlaAspAlaHisTrpThrGly 21
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; TITLE OF INVENTION: NON-STEROIDAL ESTROGEN-RECEPTOR
; TITLE OF INVENTION: NON-STEROIDAL ESTROGEN-RECEPTOR
; TITLE OF INVENTION: AND GOOD STEROIDAL
; TITLE OF INVENTION: AND GOOD STEROIDAL
; CURRENT APPLICATION NUMBER: US/09/773,816
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/243,458
; PRIOR APPLICATION NUMBER: US 60/179,305
; PRIOR FILING DATE: 2000-10-25
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                 2199603 TGCGGTCGACCGCGTGG-ATT-----TGCGGTTTCTCG-
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09773816
Patent No. 6340774
GENERAL INFORMATION:
APPLICANT: Stanford University
APPLICANT: Khosla, Chaitan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O
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; OTHER INFORMATION: n = A,T,C or
US-09-773-816-1
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Best Local Similarity:
Query Match:
                                             Percent Similarity:
Best Local Similarity:
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 1
LENGTH: 23673
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US-09-773-816-1
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                                                                                    Query Match:
DB:
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Fatent No. 6294328
GENERAL INFORMATION
APPLICANT: FLEISCHAM, Robert D.
APPLICANT: FRASER, Claire M.
APPLICANT: WHITE, Owen R.
APPLICANT: WHYER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: TUBENCULOSIS
TITLE OF INVENTION: TUBENCULOSIS
FILE REPRENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT APPLICATION NUMBER: US/09/103,840A
SOFTWARE: PATENTIN OF: 2.1
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OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
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APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NGS: 2 998-06-24
SEQ ID NO 2
LENGTH: 4403765
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Mycobacterium tuberculosis
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US-09-103-840A-1
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APPLICANT: SCHLOKAT, Uwe
APPLICANT: FISCHER, Bernhard
APPLICANT: FISCHER, Falko-Guenther
APPLICANT: FALKNER, Falko-Guenther
APPLICANT: FORNER, Friedrich
APPLICANT: DORNER, Friedrich
APPLICANT: DORNER, FRIEDRICH
APPLICANT: DORNER, FRIEDRICH
APPLICANT: BIBL, Ochann
TITLE OF INVENTION: DERIVATIVE OR A DERIVATIVE OF A FURIN ANALOGUE AND A
TITLE OF INVENTION: HETEROLOGOUS SEQUENCE
                                                                                                                                                      615 Geccaacaacegrererereragereridaeceracaacececedaridaaeeegrece 674
                                                                                                                                                                                                                                                            735 CCACATCCACATCTACAGTGCCAGCTGGGGCCCCGAGGATGACGGCAAGACAGTGGATGG 794
                                                                                                                                                                                                                                                                                                                                             ---SerArgTrp 50
                                                                                                3 GlyArgProArgArgValSerAlaGlyCysGlyPheAlaAspAlaHisTrpThrGlyLeu 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----SerAla 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 GlyLeuThrValArgAspArgProGlnLeuGlyGluLeuCysMetGlyArgGly
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STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
CITY: Washington
COUNTRY: USA

ZIP: 20007-5109
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/753,247
FILING DATE: 22-NOV-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: AT 1928/95
FILING DATE: 24-NOV-1996
FILING DATE: 24-NOV-1997
FILING DATE: 24-NOV-1996
                                                                                                                                                                                                                   23 TrpThrGly---LeuGlyGluGlyGlnGluGlyGly-
                                      US-09-972-032-2 (1-79) x US-08-753-247-13 (1-1758)
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CORRESPONDINGE ADDRESS: Electric Landler
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                         40 AlaSerProThrProAspCysAla----
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INFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS: LENGTH: 1776 base pairs TVPE: nucleic acid
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18586 TCGGGCTCGGCGCGTCTGCGGCACCGCCCCGGCGAGTTGTCCGGCGGGCAGCAGCAGC 18645
                                                                                                                         -- CGCGCGCCTGGTCAGCA 18675
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APPLICANT: SCHLOKAT, Uwe
APPLICANT: FISCHER, Bernhard
APPLICANT: FISCHER, Falko-Guenther
APPLICANT: FALKO-Guenther
APPLICANT: DORNER, Fractich
APPLICANT: DORNER, Fractich
APPLICANT: DIBL, Johann
TITLE OF INVENTION: DERIVATIVE OR A DERIVATIVE OF A FURIN ANALOGUE AND A
TITLE OF INVENTION: DERIVATIVE OR A DERIVATIVE OF A FURIN ANALOGUE AND A
TITLE OF INVENTION: HETEROLOGOUS SEQUENCE
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                61
                                                         42 ProThrProAspCysAlaSerArgTrpProArgSerAlaSerArgTrpProTrpSerAla
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ZIP: 20007-5109
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/753,247
FILING DATE: 22-NOV-1996
CLASSIFICATION ADATA:
APPLICATION NUMBER: AT 1928/95
FILING DATE: 24-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 40433/149
FERERENCE/POCKET NUMBER: 40433/149
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Matches:
Conservative:
Mismatches:
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Patent No. 6210929
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1758 base pairs
TYPE: nucleic acid
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LOCATION: 1..1
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US-08-753-247-13
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1794 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) FEATURE:
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Sequence 20, Application US/08753247

Sequence 20, Application US/08753247

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ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFBRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/753,247
FILING DATE: 2-NOV-1996
CLASSIFICATION: 435
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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APPLICATION NUMBER: AT 1928/95
FILING DATE: 24-NOV-1995
ATTORNEY/AGENT INFORMATION:
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Matches:
Conservative:
Mismatches:
Indels:
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Percent Similarity:
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NAME/KEY:
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LOCATION:

US-08-753-247-20
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                               FEATURE:
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July 10, 2004, 16:36:45 ; Search time 2885 Seconds (without alignments) 817.717 Million cell updates/sec
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GenCore version 5.1.6
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Listing first 45 summaries
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B ID	111 BCC039500 12 BNA406138 12 BNA406138 13 BNA606138 13 BNA606108 12 BNA606108 12 BNA606108 13 BUG20427 14 CD742581 13 BUG171626 12 BC64336 12 BC64336 12 BC64336 13 BC997672 14 CD771628 13 BC9675995 14 CB675995 14 CB675995 14 CB675995 14 CB675995 15 BC675995 16 BC776603 17 BC67899 18 BC776603 19 BC776603 10 BC776603 11 BC776603 11 BC776603 12 BC7760829 14 CB671698 15 BC7760829 16 BC7760829 17 BC776603 18 BC776603 19 BC776603 10 BC776603 11 BC7760829 10 BC7760829 10 BC7760829 11 BC7760829 11 BC7760829 11 BC7760829 12 BC77760829 13 BC777760829 14 CB6777698 15 BC777777 16 BC77777 17 BC7777 18 BC777 18 BC7777 18 BC7777 18 BC777	a; Chordata; Craniata; Ve a; Primates; Catarrhini; 67)
Ω,	1467 1 1684 1 1684	nomo saplens Eukaryota; Metazoa Mammalia; Eutheria 1 (bases 1 to 146' Strausberg,R.
Result Score	44 4 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	OKGANISM HO EV MA REFERENCE 1 AUTHORS St

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Homo sapiens
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Best Local Similarity:
Query Match:
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     AUTHORS
TITLE
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COMMENT
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                                                                                                                          Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the 1.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 88 Row: g Column: 1 This clone has the following problem: retained intron. Location/Qualifiers
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               Submitted (01-NOV-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 1201)
                                                                                                                                                                                                                                                          Contact: (Dickson, Mark) mcdopaxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     853 GCAGGICTIACCGICCGAGAICGICCGCAACIGGGCGAGCIGIGCAIGGGGCGIGGC 909
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/mol_type="manny",

/db xref="taxon:9606"

/clone="IMAGE:555626"

/tissue_type="Uterus, leiomyosarcoma"

/clone_lib="NIH MGC_71"

/lab_host="DH10B"
                                                                                          NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Matches:
Conservative:
Mismatches:
Indels:
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   Direct Submission
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Best Local Similarity:
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KEYWORDS
SOURCE
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                                                                                                            COMMENT
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BM980506
UI-CF-EN1-add-a-08-0-UI.sl UI-CF-EN1 Homo sapiens cDNA clone
UI-CF-EN1-add-a-08-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev stage="fetal"
/clone_lib="Homo sapiens FETAL LIVER"
/clone_logan: liver; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECORV sites of the pCMVSPORT 6 vector. Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         653 GGGCTCTGGACTGGGCTAGGGGAAGGCCAGGAGGCGGAATTGCCCCGAG-GGCCAGGCC 595
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                                                                                                                                                                                                                                                                       http://www.genoscope.cns.fr/
cgi.bin/cluster.ggiSeq=CSOAM010CB10NPl&cluster=8395.f. Contact
cgi.bin/cluster.cgiSeq=CSOAM010CB10NPl&cluster=8395.f. Contact
Feng Liang Email: fliang@lifetech.com/ URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOAM010CB10NPl.
Location/Qualifiers
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MetCysGlyArgProArgArgValSerAlaGlyCysGlyPheAlaAspAlaHisTrpThr
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8395.f
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AlaGlyLeuThrValArgAspArgProGlnLeuGlyGluLeuCysMetGlyArgGly
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Matches:
Conservative:
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/tissue_type="FETAL LIVER"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels:
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TITLE
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us-09-972-032-2_1.rst

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 691)

1 (bases 1 to 691)

1 NGI-GGAP http://www.nobi.nlm.nih.gov/ncicgap.

NGI-GGAP http://www.nobi.nlm.nih.gov/ncicgap.

NGI-GGAP http://www.nobi.nlm.nih.gov/ncicgap.

I unnor dene Index

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-ramail.nih.gov

Tissue Procurement: James Martin

CDNA Library Parayed by: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained Seg primer: Mls FORMARD

POUNA=Yes.
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UI-H-FLI-bfw-n-19-0-UI.S1 NCI_CGAP_FLI Homo sapiens CDNA clone
UI-H-FLI-bfw-n-19-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 GlyGluGlyGluGlyGlyIleGlyProGluGlyGluGlyGlnAlaSerProThrProAspCys 46
579 GTCCGAGATCGTCCGCAACTGGGCGAGCTGTGCATGGGGCGTGGC 535
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Conservative:
Mismatches:
Indels:
Gaps:
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BU620427.1 GI:23286642
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274.00
98.11%
98.11%
60.09%
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Homo sapiens
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KEYWORDS
SOURCE
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                                                                                  RESULT 4
BU620427/c
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AUTHORS
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Jeb host="DH10B (Life Technologies) (T1 phage resistant)"

Jelon lib="UI-CF-ENI"

Jelon lib="UI-CF-ENI"

Jelon lib="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;

UI-CF-ENI is a normalized CDNA library containing the following tissue(s): Primary Lung Cystic Fibrosis

Epithelial Cells. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-866, 1996. First strand CDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded CDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT) 18 tail. The sequence tag for this library is CTGCTCAGGT.

TAG LISSUB=Human Lung Epithelial Cell Lines untreated LPS Ghr ToEP SYRM
TAG LIB=UI-CF-ENI

                                                                                                        MCCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com)
Seg primer: M13 FORWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Docation/Qualifiers

1. 760

/organism="Homo sapiens"

/mol type="mRNA"

/db Xref="taxon:9606"

/clone="Ul-CF-EN1-add-a-08-0-Ul"

/closue type="Frimary Lung Cystic Fibrosis Epithelial

/cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G.
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Matches:
Conservative:
Mismatches:
Indels:
  Genome Res. 6 (9), 791-806 (1996)
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Contact: McCray, PB
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Best Local Similarity:
Query Match:
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  JOURNAL MEDLINE PUBMED COMMENT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.

B. (Bases 1 to 1084)

B. (Bases 1 to 1084)

NHH-MGC http://mgc.noi.nih.gov/.

L. Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, inc.

CDNA Library Preparation: Life Technologies, inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://image.llnl.gov

Plate: LLAM12276 row: b column: 11

High quality sequence stop: 672.
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AGENCOURT_6553891 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5555626
5', mRNA sequence.
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/organism="Homo sapiens"
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       TAG_SEQ=CTGCTCAGGT"
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Best Local Similarity:
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/lab_host="DH10B (life Technologies) (T1 phage resistant)"
/clone lib="UI-CF-ENI"
/clone lib="UI-CF-ENI"
/note="Grgan: Lung; Vector: PT713-pac (Pharmacia) with a modified polylinker; Site 1: ECOR 1; Site 2: Not 1;
UI-CF-ENI is a normalized_cDNA library containing the following tissue(s): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA syntheeis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I i, and cloned directionally into pT773-pac vector. The
                                                                                                                                                                                                                                                                                                                                                                                                                BUG684594 694 bp mRNA linear EST 07-OCT-2002
ULCF-EN1-act-a-22-0-UI.s1 UL-CF-EN1 Homo sapiens cDNA clone
UI.CF-EN1-act-a-22-0-UI 3', mRNA sequence.
BU684594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: paul-mocray@niowa.edu

Isasue Procurement: Dr. M. J. Welsh, University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CLONE Distribution: Researchers may obtain clones from Research

Genetics (www.resgen.com) or from Open Biosystems

Seq primer: MI3 FORWARD

POLYA=Yes.
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TAG_IISSUB=Human Lung Epithelial Cell Lines untreated LPS
                                                                                                         630 GCCTCCCGGTGGCCCCGCAGCGCCTCGGAGTGCAGGTCTTACCGTCCGA 571
689 GGGGAAGGGCAGGAGGCGGAAT-GGGCCCGAGGGCCAGGCCTCGCCGACCCCCGACTGC 631
                                                                        99
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                          47 AlaSerArgTrpProArgSerAlaSerArgTrpProTrpSerAlaGlyLeuThrValArg
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/clone="UI-CF-ENI-act-a-22-0-UI"
/tissue_type="Primary Lung Cystic Fibrosis Epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University of Iowa 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA Tel: 319 356 4866 Fax: 319 356 7171
                                                                                                                                                                                                                                                              570 GATCGTCCGCAACTGGGCGGGCTGTGCATGGGGCGTGGC 532
                                                                                                                                                                                                    67 AspargProGlnLeuGlyGluLeuCysMetGlyArgGly 79
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TAG_LIB=UI-CF-EN1
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McCray Lab
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/mol_type="mRNA"
/mol_type="mRNA"
/db xref="taxon:9606"
/clone="UI-H-DF0-bep-n-09-0-UI"
/tissue_type="subchondral Bone"
/dev_stage="Adult"
/lab_host="DH10B" (Life Technologies)"
/clone_lib="NCI_CGAA_DF0"
                                                                                                                                                                                                                                                    Conservative:
Mismatches:
Indels:
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Matches:
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University of lowa
University of lowa
375 Newton Road, 4156 MEBRF, lowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-coares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA-Yes:
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BM679577
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852 CCTGGGAGGCAAGGCTTTACCCGTCCCCAAATCGTCCCCAACCTGGGGGAAATTGTGGCT 911
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                               39 nAlaSerProThrProAspCysAla-SerArgTrp-ProArgSerAlaSerArgTrp--P
                               1 MetCysGlyArgProArgArgValSerAlaGlyCysGlyPheAlaAspAlaHisTrpThr
                                                                                         21 GlyLeuTrpThrGlyLeuGlyGlu-GlyGlnGluGlyGlyIle---GlyProGluGlyGl
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US-09-972-032-2 (1-79) x BM806108 (1-1084)
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Homo sapiens
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AUTHORS
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MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
SOURCE
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In (JOSES I TO 0.324)

NOI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Tagaphs-Indingov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library Parayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@ulowa.edu
with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pTT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGGTATACC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI). TAG ILSUE-human fetal eye Institute (NEI).

TAG ILSE-LI-E-BOO TAG_SEQ-CGGGTATACC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              669 GAGGGCCAGGCCTCGCCGACCCCCGANTGCGCCTCCCGGTGGCCCCGCAGCGCCTCCCGG 610
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 632)

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/note="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR 1; Site 2: Not 1; NCI CGAP DF0 is a cDNA library containing the following tissue(s): Subchondral Bone. The library was constructed according to Bonaldo, Lennon and Soarse; Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dr primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and clonned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTTAAGCGTC.
TAG_INB-UI-H-DF0
TAG_INB-UI-H-DF0
TAG_ESCG-GTTAAGCGTC"
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2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 4866
Fax: 319 and Tel: 319 366 7171
Email: paul-mccray@wilowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Matches:
Conservative:
Mismatches:
Indels:
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Seg primer: M13 FORWARD
POLYA=Yes.
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CA313142,1 GI:24531240
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187.00
100.00%
100.00%
41.01%
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Best Local Similarity:
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DB:
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VERSION
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TITLE
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a 8 ద Location/Qualifiers

source

FEATURES

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/d_xel="taxcoligous"
/d_xel="taxcoligous"
/dloxe=tul-Garcoligous
/tissuc type="Human Lung Epithelial cells"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/dlone_lib="UL-CP-RNO"
/dlone_lib="UL-CP-RNO"
/dlone_lib="dul-CP-RNO"
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/dlone_lib="dul-CP-RNO"
/dlone_lib="dul-CP-RNO"
/dlone_lib="dul-CP-RNO"
/dlone_lib="dul-CP-RNO"
/dlone_lib-ray description libraries (En1 and D1) The library was subtracted according to according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, bento-soares@ditional information, contact:
/d_TISSUE=Human Lung Epithelial Cell Lines untreated LPS
fhr to LPS 24h
TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS
fhr to LPS 24h
TAG_SEQ=CTGCTCAGGT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
Seq primer: Ml3 FORWARD
POLYA-Yes.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
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/db_xref="t=axon_9606"
/db_cref="t+axon_9606"
/dbone="U-HFT2-bjl-i-10-0-UI"
/tissue="U-HFT2-bjl-i-10-0-UI"
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Mismatches:
Indels:
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Matches:
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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CD742581.1 GI:32293431
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Homo sapiens
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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
       NCI CGAP_Ctl is a normalized cDNA library containing the following tissue(s): Osteoarthritic Cartilage The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, dispeted with Not I, and cloned directionally into pT713-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the manner.
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(Dases 1 to 486)
Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,
Pahrenkrug,S.C., Wise,T., Rohrer,G.A., Pertea,G., Sultana,R.,
Quackenbush,J. and Keele,J.W.
Porchne gene discovery by normalized cDNA-library sequencing and Bast cluster assembly
Mamm. Genome 13 (8), 475-478 (2002)
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537701 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
BM484011
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TAG_LIB=UI-H-EUI
TAG_SEO=TGATCACGCT"
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Matches:
Conservative:
Mismatches:
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/wol_type="mRNA"
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BACKWARD: GTTTCCCAGTCACGACG
Plate: 2 row: K column: 16
Seg primer: ATTTAGCTGACACTATAG.
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Best Local Similarity:
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DB:
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/dev_stage="Adult"
/lab_host="NHIOB (Life Technologies)"
/lab_host="NHIOB (Life Technologies)"
/clone_lib="NCI_CGAP_FT2"
/noce="Organ: Ling; Vector: pT7T3-Pac (Pharmacia) with a modified poly; linker; Site_1: ECOR I; Site_2: Not I;
NCI_CGAP_FT2 is a subtracted constituted from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. TAG_TISSUE-Human Lung Aveolar Macrophage
TAG_LIB-UI-H-FT2
TAG_ESO-GGCCATGCCG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: capabs.ramail.ih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@wiowa.edu
POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BQ447041 628 bp mRNA linear EST 28-MAY-2002 UL-H-EU1-bac-p-06-0-UI.S1 NCI CGAP Ct1 Homo sapiens cDNA clone UL-H-EU1-bac-p-06-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol type="many" | mol type="many" | mol type="many" | mol type="many" | db xref="taxon:966" | clone="Ul-H-EUI-bac-p-06-0-UI" | tissue type="Osteoarthritic Cartilage" | dev_stage="Adult" | clife Technologies | mol tise="tayon" | clife Technologies | clife Technologies | clone lib="NCI CGAP CII" | clone lib="NCI CGAP CII" | note="Organ: Knee; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 628)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 SerArgTrpProArgSerAlaSerArgTrpProTrpSerAlaGlyLeuThrValArgAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ArgProGlnLeuGlyGluLeuCyaMetGlyArgGly 79
                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
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/organism="Homo sapiens"
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BQ447041.1 GI:21250153
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Unpublished (1997)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
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BQ447041/c
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AUTHORS
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BQ644396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    524 bp DNA linear GSS 17-JUN-2003 CH240 359W23.T7 CHORI-240 Bos taurus genomic clone CH240_359M23, penomic survey sequence.
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Holt.R., Stott,J., Yang,G., Barber,S., Smailus,D., Prabhu,A.-L.,
Tsai,M., Cloutier,A., Lee,D., Girn,N., Olson,T., Mayo,M.,
Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A., Chiu,R.,
Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S.,
Sobein,J., Marra,M., de Jong,P., McWilliam,S., Barris,W.,
Dalrymple,B.P. and Tellam,R.
Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
Other GSSs: CH2035
Other GSSs: CH20359M23.TARBACI3P2
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26
                                                       /clone_lib="MARC 2PIG"
/note="Wetcor: pCMV SPORT6, Site_1: Not1; Site_2: Sal1;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 uGlyGlnAlaSerProThrProAspCysAlaSerArgTrpProArgSerAlaSerArg--
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Exax: 604-877-6276
Email: rholt@bcgsc.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323 IGGICITGGGIGGCCGIGGCTITITGGGIGGIAIGGCAGGAACAGA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------TrpProTrpSerAlaGlyLeuThrValArgAspArg 68
                                                                                                                                                                                                       448
222
220
300
400
                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
               /tissue_type="pooled"
/lab_host="DH108"
db xref="taxon:9823"
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98.50
44.74%
38.16%
21.60%
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Bos taurus
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DB:
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1362 bp mRNA linear EST 15-JUL-2002
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 GlyGluGlyGluGlyGlyIleGlyProGluGlyGlnAlaSerProThrProAspCys
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Tissue Procurement: CGAP (Stanford)

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47 AlaSerArg-----TrpProArgSerAlaSerArgTrpPro----
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Mismatches:
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Matches:
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/strain="breed: Hereford"
                                                                                                                                                                   1. .524
/organism="Bos taurus"
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/clone="CH240_359M23"
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BQ644396.1 GI:21768568
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Plate: 359 row: |
Seq primer: T7
Class: BAC ends.
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                                                    BG539339 872 bp mRNA linear EST 03-APR-2001
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Homo sapiens (human)

Exaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mational Institutes of Health, Mammalian Gene Collection (MGC)

Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: capabs-rémail.nih.gov,

CONTECH Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Genomics, Inc.

CLONG distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 ThrGlyLeuGlyGluGlyGluGlyGlyIleGlyProGluGlyGlnAlaSerProThr 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 ProAspCysAlaSerArgTrpProArgSerAlaSerArgTrpProTrpSerAlaGlyLeu 63
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29
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Matches:
Conservative:
Mismatches:
Indels:
  07
Plate: LLCM2482 row: m column:
High quality sequence start: 65
High quality sequence stop: 380.
Location/Qualifiers
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38.16%
21.16%
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Best Local Similarity:
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BG539339
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AUTHORS
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8 요 à a d 슝 a ò 염

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/mol_type="mRNA"
/db_ref="taxon:9606"
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/clone lib="NIH MGC 77"
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/note="Organ: lung' vercor: pDNR-LIB (Clontech vercor: power); Vercor: power)
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Job time : 2893 secs
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AC135044 Homo sapi
AK110169 Oryza sat
AC006405 Homo sapi
S53698 tal-1=exons
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AC117415
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AE016915
AE016913
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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THEADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
                                                                                                           ; Search time 2821 Seconds (without alignments) 1213.789 Million cell updates/sec
                                                                                                                                                                                                                      1 MCGRPRRVSAGCGFADAHWT.....SAGLTVRDRPQLGELCMGRG
   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                          nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                         3470272 seqs, 21671516995 residues
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
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                                                                                          Homo sapiens
SEQUENCE, 22
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  AC135050 182230 bp DNA linear PRI 27-FEB-2003
Homo sapiens chromosome 16 clone RP11-196G11, complete sequence.
AC135050
                                                                                                                                                                                                                                                                                                                                    Unpublished

2 (bases 1 to 182230)

DOE Joint Genome Institute.

Submitted (05-OCT-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                www.jgi.doe.gov
Pinishing Completed at Stanford Human Genome Center and Los Alamos
National Laboratory
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Submitted (22-007-2002) Production Sequencing Facility, DOB Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA (bases 1 to 182230)

Mobb Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.

Direct Submission
                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 182230)
DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (27-FEB-2003) DOB Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Feb 27, 2003 this genence version replaced gi:24211094. Draft Sequence Produced by DOB Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MetCysGlyArgProArgArgValSerAlaGlyCysGlyPheAlaAspAlaHisTrpThr 20
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/or__type="ganomic DNA"
/db_xref="taxon:9606"
/chromosome="t6"
/clone="RP11-196G11"
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195476 bp DNA linear HTG 05-OCT-2002 chromosome 16 clone CTD-2551B20, WORKING DRAFT unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (05-OCT-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
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1 (Dases 1 to 195476)

DOB Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished

2 (Dases 1 to 195476)

DOB Joint Genome Institute.
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contig of 1509 bp in length
gap of unknown length
gap of unknown length
contig of 1850 bp in length
contig of 1850 bp in length
gap of unknown length
contig of 1136 bp in length
gap of unknown length
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1302: gap of unknown length
2468: contig of 1166 bp in length
2568: gap of unknown length
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gap of unknown length
contig of 5717 bp in length
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bp in length
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HTG; HTGS PHASB1; HTGS_DRAFT; HTGS_ACTIVEFIN.
Homo sapiens (human)
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contig of 1993 bp in
gap of unknown leng
contig of 2490 bp in
gap of unknown leng
contig of 3997 bp in
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contig of 6084 b
gap of unknown l
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URL: http://cdnaol.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satch,K.,
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satch,K.,
Inhikawa,M., Yamada,H., Oboi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Oboi,H., Hotta,I., Kojima,K., Namihi,T.,
Ohneda,E., Yahagi,M., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y.,
Fujimura,T., Kussumegi,T., Lu,M., Masuda,H., Mura,J.,
Mizuno,K., Narikawa,R., Ishibiki,J., Kawamata,M., Kobayashi,M.,
Kodama,T., Kursoaki,T., Kusumegi,T., Lu,M., Masuda,H., Mura,J.,
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Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S.,
Genome Exploration Research Group in Riken Adachi,J., Aizawa,K.,
Akmura,T., Arakawa,T., Carninci,P., Fukuda,S., Hangaki,T.,
Harao,A., Hashizume,W., Hayashida,K., Hayatsu,N., Harancto,K.,
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Noya,S., Kurihara,C., Matsuyama,T., Niyazaki,A., Murata,M.,
Nishi,K., Nomuza,K., Numagama,J., Xakazume,N.,
Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Takahashi,F.,
Takatu-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,
Takatu-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,
Yasunishi,A. and Hayashizaki,Y.
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Science Genome Sequencing & Analysis Group:, Otomo,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Kusuosaki,T., Masuda,H., Kobayashi,M., Yise,Q., Lu,M., Marikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J., Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Mizua,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,R., RIKEN:, Kayama,J., Carninci,P., Adachi,J., Alazwa,K., Arakawa,T., Fikuda,S., Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y., Saito,R., Sasaki,D., Sato,K., Shibata,R., Shinagawa,A., Shiraki,T., Collection, mapping, and annotation of over 28,000 cDNA clones from imponica rice
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Submitted (27-AGG-2002) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
205-6602, Japan (E-mail:sKikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fas.81-29-838-7007, This clone is one of the 28K full-length cDNA clones from japonica
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Oryza sativa (japonica cultivar-group) cDNA clone:002-161-G03, full insert sequence.

AK110169

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AK10
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    48370: contig of 9267 bp in length 48470: gap of unknown length 59821: contig of 11251 bp in length 72304: contig of 11251 bp in length 72304: gap of unknown length 72404: gap of unknown length 85349: contig of 12945 bp in length 101872: contig of 12945 bp in length 101872: contig of 16423 bp in length 101972: gap of unknown length 11706: gap of unknown length 11706: gap of unknown length 118973: contig of 15104 bp in length 118973: contig of 12104 bp in length 118973: contig of 12104 bp in length 118036: contig of 11263 bp in length 150336: contig of 11263 bp in length 150336: contig of 11263 bp in length 150436: contig of 45040 bp in length 195436: contig of 45040 bp in length
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Wheeler, J., Wu.X., Wyman, D., Ye, W.J. and Zody, M.

Direct Submission

Submitted (15-7M-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jan 21, 1999 this sequence version replaced gi:4159875.

All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997).

**NOTE: This is a 'working draft' sequence. It currently consists of 12 condigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are unknown.

**This record will be updated with the finished sequence is as soon as it is available and the accession number will
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12285: contig of 3470 bp in length
12285: contig of 3470 bp in length
40956: contig of 28671 bp in length
gap of unknown length
64393: contig of 23437 bp in length
78975: contig of 1482 bp in length
gap of unknown length
gap of unknown length
96637: contig of 1482 bp in length
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gap of unknown length
10 163035: contig of 2056 bp in length.
Location/Qualifiers
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/clone_lib="RPCI-11 human BAC library"
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/organism="Homo sapiens"
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/chromosome="17"
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Homo sapiens chromosome 17 clone hRPK.107 N 19 map 17, ***
SEQUENCING IN PROGRESS ***, 12 unordered pieces.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                           /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivar="Nipponhare"
/db ref="taxon:39947"
/clone="002-161-G03"
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1 (bases 1 to 163035)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Bron sapiens chromosome 17, clone hRPK.107_N_19
Unpublished
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42
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Mismatches:
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HTG; HTGS PHASE1.
Homo sapiens (human)
Homo sapiens
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AC006970 136098 bp DNA linear PRI 15-OCT-2003
Homo sapiens PAC clone RP4-725G10 from 7, complete sequence.
AC006970
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Submitted (05-MAR-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
Mo 3108, USA
4 (bases 1 to 136098)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence of this clone was established as part of a mapping and sequencing collaboration between the NiGKI Chromosome 7 Mapping project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see thtp://www.nhgri.nih.gov/DIR/GTB/GTR7, send mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (27-SEP-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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This clone was derived from human PAC library RPCI-4, prepared by
Pieter de Jong and coworkers at http://www.chori.org.using the
                                                                                                                                                                                                                                                                                         Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (15-OCT-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63 On Sep 27, 2000 this sequence version replaced gi:9838025.
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Du,H., Haakenson,B. and Stoneking,T.
The sequence of Homo sapiens PAC clone RP4-725G10
Unpublished (2001)
3 (bases 1 to 136098)
Waterston,R.H.
                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 136098)
Sulston, J.E. and Wilson, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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5 (bases 1 to 136098)
Wilson, R.
Direct Submission
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DNA [human, HEL cell line, Genomic,
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Exon la (nt 256-379) and exon lb (nt 657-890) are involved in alternative splicing of tal-1 gene.

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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11-1=exons la, lb and flanking 1
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SSAAAPRQPGLMAQWATTAAGVAVGSAVGHTLGHAITGGFSGGSNAEPARPDITYQEP
QGTQPAQQQQPCLYEIKQFLECAQNQGDIKLCEGFNEVLKQCRLANGLA"
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                                                                                                                        complement (join (7112. .7398,8404. .8548,9763. .10012, 11901. .12011))
/gene="LOC51142"
complement (join (7388. .7398,8404. .8548,9763. .10012, 11901. .11950)]
/gene="LoC51142"
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complement(join(7110, .7398,8404. .8548,9763, .10012, 11901, .11987)
/gene="LOC51142"
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17pt family="MIR"
12823. .12946
17pt family="L2"
12990. .13272
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|protein_id="AAQ96886.1"
|db_xref="GI:37674436"
       complement (7106, .12011)
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/rpt_family="Alu"
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/rpt_family="Alu"
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11030_..1137
/rpt_family="Alu"
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                                                                                                                NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-782E10 the clone sequenced
to the right is RP11-700P18. Actual start of this clone is at base
position 1 of RP4-725G10 actual end is at base position 136098 of
RP4-725G10.
method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor. The clone may be obtained either from Genome Systems, Inc. (http://www.genomesystems.com) or Research Genetics, Inc. (http://www.resgen.com); or from Pieter de Jong.
                                                                                                                                                                                                Location/Qualifiers
1. 136098
1. Grganism="Homo sapiens"
| Mol_type="genomic DNA"
| db xref="taxon:9606"
| chromosome="7"
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7.pt_family="Alu"
5480. 5545
7.pt_family="MBR2_type"
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/rpt_family="Alu"
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018. .4187
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1704. 2000
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4664. .4963
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195-
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US-09-972-032-2 (1-79) x AF164165 (1-2163)	5 ProArgArgValSerAlaGlyCysGlyPheAlaAspAlaHisTrpThrGlyLeu	430 CCTAGGCATGGACTGGAGGCTTTGGGATGGACTGAGAGGCACTGGAAGGGAGTGGGAGAG	Qy 23	32 G17	Db 310 GGACTGRRAGGVGMNGRTTMGACTGGGATTGGCTGGGATGGTCACTGGCAGGCAGGCCC 251	Qy 37 GludlyGlnAlaSer	42		130 CGCIGIT	Oy 70 Gin 70 1:: Db 70 CGT 68	AC092012 153675 bp DNA linear HTG	DEFINITION Felis catus clone RP86-89F20, WORKING DRAFT SEQUENCE, 5 unordered	ACCESSION AC092012. VERSION AC092012.1 GI:14389334 KEYWORDS HTG: HTGS PHASE1: HTGS DRAFT.	SOURCE Felis catus (cat) ORGANISM Felis catus	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Carnivora; Fissipedia; Felidae; Felis.	AUTHORS Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W.,	Boulfard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupte, J., Ho, SL., Idol, J.R., Karlins, E., Lee-Lin, SQ., Legaspi, R., Lim, M., Maduro, Q.L., Maduro, V.B.,	Masiello,C., Mastrian,S.D., McCLoskey,J.C., McDcwell,J.J., Pearson,R., Praead,A., Shevchenko,Y., Snyder,B., Stantripop,S., Thomas T W Thomas D T Molhwar T W Teirrach C Wort T L	Malker, MA., Wetherby, K.D., Zhang, LH. and Green, B.D. TITI: NISC Comparative Seminancing Initiative	Unpub	AUTHORS Green, E.D. TITLE Direct Submission JOURNAL Submitted (13-JUN-2001) NIH Intramural Sequencing Center, 8717	Grovemont Circle, Gaithersburg, MD 20877, USA COMMENT Genome Center	Center: NIH Intramural Sequencing Center Center code: NISC	Web site: http://www.nisc.nih.gov Contact: nisc_mouse@nhgri.nih.gov	Center project name: cfb	Sequencing Vactor: plasmid; 100% of reads	Assembly program: Phrap; version 0.990319 Consensus quality: 157010 bases at least Q40 Consensus quality: 11335 bases at least Q30 Consensus quality: 151627 bases at least Q20
	Oy 36	Qy 44 oAspCysAlaSerArgTrpProArgSerAlaSerArgTrpProTrpSerAlaGlyLeuTh 64	80530 GGGCGCTCCTCACGGGTGGTCCAGGCTAGC	64 rValArgAspArgPr 69	08408	GCAAGTACCACGGACCTCCTCCGGCCTCGGC	RESULT 7 AF164165/C LOCUS AF164165 2163 bp DNA linear VRT 13-MAR-2000 DEFINITION Certhidea olivacea MHC class IIB antigen gene, partial cds.	. GI:6941861	Certhidea olivacea SM Certhidea olivacea	<pre>Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Passeriformes; Passeroidea; Fringillidae; Emberizinae; Certhidea.</pre>	REFERENCE 1 (Dases 1 to 2163) AUTHORS Sato,A., Figueroa,F., Mayer,W.E., Grant,P.R., Grant,R. and Klein,J. TITLE MHC class II genes of Darwin's Finches: Divergence by point mutations and reciprocal recombination	JOURNAL (in) Kasahara,M. (Ed.); MAJOR HISTOCOMPATIBILITY COMPLEX. EVOLUTION, STRUCTURE, AND		TITHE Direct Submission	н	FEATURES Location/Qualifiers source 12163	/organism="Certhidea Olivacea" /mol rype="genomic DNA" /isolare="D1103-12"	/db_xref="taxon:48880" 	/product="MHC class lib antigen" join(<1, 223, 2652, .>2163) /actolifroum 3-21	/codon start=1 /product="MHC class IIB antigen"	/potein id="AAF32250.1" /db_xref="q1:694866" /translation="TEKYRYVHREIYNRLMHVMFDSDVGHYVGFTPYGERVAXHMNSD	PAILEDRRAQVDTLCRHNYEVSRPFITERRVPPSVSISLVPPSSSQPGPRPPALLRDG FLPCPDPGEV"	exon <1223 /number=2	exon 2052. >2163 /number=3	į	307 Length: 98.50 Matches:	refcent Similarity: 32.23% Conservative: 3 Dest Local Similarity: 28.10% Mismatches: 27 Query Match: 21.60% Indels: 55 DB: 6

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153278 GCCCTGGAAGAAGGAGTCCGCGGTCCGCGGGGGGCAAAGGTTCCCGATCGGGGGAGGGCG 153337
                                                                                                                                                                                                                                             AC134385 185997 bp DNA linear HTG 27-NOV-2003
Papio anubis clone rp41-10512, WORKING DRAFT SEQUENCE, 2 ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Papio.

1 (bases 1 to 18597)

Commen, S., Shaikh, T. and Roe, B.A.

Papio anubis BAC Clone rp41-10512

Unpublished

2 (bases 1 to 18597)

Commen, S. and Roe, B.A.

Direct Submission

Submitted (26-SEP-2002) Department Of Chemistry And Biochemistry, Chemistry of Oklahoma, 620 Parrington Oval, Room 208, Norman, Chemistry of Oklahoma, 620 Parrington Oval, Room 208, Norman, Chemistry of Oklahoma, 620 Parrington Oval, Room 208, Norman, Chemistry
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(Description of the control of the c
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/db_xxef="taxon:9555"
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* This sequence will be replaced

* by the finished sequence as soon as it is available and

the accession number will be preserved.

* 118469 118568: gap of 118468 bp in length

* 118569 18559: contig of 67429 bp in length.
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Mismatches:
Indels:
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Matches:
                                                                                                                      153338 GGGGGCTGTGGACGGGCAGGGGC 153361
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                                                                                                                                                                                                                                                                                                                                 AC134385
AC134385.10 GI:38564357
HTG; HTGS_PHASE2; HTGS_DRAFT.
Papio anubis (clive baboon)
                                                             GlyGluLeuCysMetGlyArgGly
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                                                             72
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KEYWORDS
SOURCE
ORGANISM
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AC134385/c
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45
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                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                         Insert size: 153275; sum-of-contigs
Quality coverage: 13.08x in Q20 bases; agarose-fp
Quality coverage: 12.28x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                        1 12153: contig of 12153 bp in length 1254 12253; gap of unknown length 2448; contig of 10195 bp in length 2548; gap of unknown length 649 46085; contig of 2353 bp in length 6186 72533; contig of 2353 bp in length 186 72533; contig of 26348 bp in length 634 72633; gap of unknown length 634 153675; contig of 81042 bp in length 614 153675; contig of 81042 bp in length 614 153675; contig of 81042 bp in length.
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Matches:
Conservative:
Mismatches:
Indels:
Insert size: 144000; agarose-fp
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72634. 153675
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/clone="RP86-89F20"
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22549. .46085
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vector_side:right"
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31.48%
27.78%
21.60%
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Nature 417 (6885), 141-147 (2002)
                                                                                                                                             (Olive) Baboon BAC Library"
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Streptomyces coelicolor A3(2) complete genome; segment 28/29.
AL939131 AL049863 AL188057 AL158060 AL158061 AL356953 AL356932 AL356932 AL590435 AL592126 AL596248 AL645882
AL939131.1 GI:24418961
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Streptomyces coelicolor A3(2)
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Streptomycineae, Streptomycetaceae, Streptomyces.
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Conservative:
Mismatches:
                                                                                                                                                - 41 Male
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Papio anubis clone rp41-111p21, WORKING DRAFT SEQUENCE, 7 ordered
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The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Papio.
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Direct Submission
Submitted (Uniosign 2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                34 IleGlyProGluGlyGlnAlaSerProThrProAspCysAlaSerArgTrpProArgSer 53
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**This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

**This sequence as soon as it is available and the accession number will be preserved.

**Sequence as soon as it is available and the accession number will be preserved.

**Sequence as soon as it is available and the accession number will be preserved.

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On Sep 11, 2003 this sequence version replaced gi:30270648
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Li,J., Yang,L., Lau,C.C.Y., Shaikh,T. and Roe,B.A.
Papio amubis BAC Clone rp41-111p21
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Li,J., Yang,L., Lau,C.C.Y., Shaikh,T. and Roe,B.A.
Direct Submission
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HTG; HTGS PHASE2; HTGS DRAFT.
Papic anubis (clive baboon)
Papic anubis
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LNRFADAAVDREVQSWVDATRRGLVTGPGTWDGYAAAAVAEAGVRALDTGVRTFVDMAP
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ELWESLERLAQLIEDGDRRELEGESSGGVTFPVRAAVNAPVRGDETAGLTDEBDVPM
DNLPPALMALNCADDPDRPTAAQVTASLDRLRARYEDVSPVFGRYRLTQVLMCYGRPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /Mote="SCSH1.36, probable protease (putative secreted protein), len: 543 aa; similar to many e.g. TR:024398 (EMBL:142758), SIDD, Streptcomyces lividans protease, (539 aa), identity in 545 aa overlap. Similar to other S.cocelicolor protease e.g. SIDD, SCRF: 02 (EMBL:AL03563) proteinse (539 aa) (35.8% identity in 545 aa overlap). Conter S.cocelicolor protease e.g. SIDD, SCRF: 02 (EMBL:AL03563) proteinse (539 aa) (45.8% identity in 545 aa overlap). Contains to entry PP00561 abhytchese, Contains Pfam match to entry PP00561 abhytchese, alpha/beta hydrolase fold, score 55.00, E-value 1.6e-12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEATDGDGGMTDPEGVLERLRDAAAECAKYSGPVLPHIGTVDAARDMDVMRRALGDDR
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(protein id="CAB43561.1"
(db_xref="G14835339"
(db_xref="G0A:Q9X7U3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="SCSH1.37, hypothetical protein, len: 364 aa;
unknown function, similar to TR:P73120 (EMB:D90903)
Synechocystis sp. hypothetical protein (358 aa), fasta
scores; opt: 492 2-score: 559.6 E(): 7.6e-24, 31.6%
identity in 364 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="SCO7254"
/note="Pfam match to entry PF01408 GFO_IDH_MOCA,
/note="Pfam match to entry PF01408 GFO_IDH_MOCA,
Oxidoreductase family, score 153.50, E-value 3.6e-42"
complement (4201. .4298)
/note="possible RBS"
/note="synonym: SC5H1.37"
complement (4404. .5498)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="synonym: SC5H1.36"
complement(5580..7211)
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/note="possible RBS"
complement (5580, .7211)
/gene="SCO7256"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (3549. .4268)
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trans1 table=11
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MGKGAMRRTLGRAEDLFVSDKADVPPPMWQTFKEEDLYGKQALAYRTLAEFEBGAA
AHAQHYADKALALRIDGRQRSKIFDYLSWASACFIADDPEQADRYARLALVSMGSNSS
ARTWDRLRQWYRLTAEYAGYPKIQELREEIKLALPKGKSPRGKGPGGTVAPA"
complement (1663, ,2979)
/gene="SCO7253"
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/db_xxef="coa.gox704"
/db_xxef="coa.gox704"
/db_xxef="coa.gox706"
/db_xxef="coa.go
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="putative regulatory protein"
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/tb_xref="SPTERME.:09X7U7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RVRRWIDMGEIPRDFVPRVLAALFTERLGRVVTIEDLGLVRHGRAGKRPHDĞSEEHPD
GVPRAPERTAAVITEFTGADLIMINKELVGAGABALAAGSARSAKHUHITDPALAAA
APDLHQPLHADPAGFRYEAAPIGSQEVEELERSVEVFRAWDAAKGGGLQRKAVUQQL
NEVGGMLAYHHPPHLQRRLWGVAANLAVLAGKWSHDVGLEPTAQKYFVIAAHAREGG
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BADYYGPAVTIGALRGHALAGTRPQRLADBLABLLALAPAVTGAVTGGYRPDTHTL
TWALASGPAPLLFRGGTGHALSGPDGPAGQDGPSGERATLEAGULLLHTGALBPEA
VEHLLTLAPRLINADSAGDGVRLVTRELDGFPGRQDACVLIARVTP"
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complement (3252. 4280)

complement (3252. 4280)

/note="SC5H1.38", probable myo-inositol dehydrogenase, len:
342 aa; similar to many e.g. SW:NIZD BACSU (EMBL:M76411),
ad, Bacillus subtilis myo-inositol 2-dehydrogenase (344
aa), fasta scores; opt: 864 z-score: 958.5 E(): 0, 38.1%
identity in 336 aa overlap. Also similar to SW:STRI_STRGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="SCEH1.40c, possible regulatory protein, len: 502
aa; similar to e.g. SW:SP15_STRGR (EMBL:M32687)
Streptomyces griseus sporulation protein (529 as;
scores; opt: 330 aa. Score: 452.2 E(): 7.2e-18, 27.9$;
identity in 530 aa. Similar to SC7A1.26 (EMBL:AL034447)
S.coelicolor possible transcriptional regulator (500 aa)
/codon startei
/transl_table=11
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complement(1663 . 2979)
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/note="SC5H1.39, hypothetical protein, len: 438 aa;
unknown function, probable CDS suggested by positional
base preference, GC frame analysis and amino acid
                                                                                                                                                                                                                                                                                                                                                                                            'note="synonym: SC5H1.40c"
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'strain="A3(2)"
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                                                                                                                                                                               db_xref="taxon:100226"
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                                                                                                                                                                                                                                                                                                            gene="SC07252"
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CDS

gene

CDS

us-09-972-032-2_1.rge

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Submitted (17-DEC-1998) Joint Genome Institute, Lawrence Livermore National Laboratory, 7000 Bast Ave., Livermore, CA 94551, USA Mational Laboratory, 7000 Bast Ave., Livermore, CA 94551, USA Mational Laboratory, 7000 Bast Ave., Livermore, Cosmid R29177 overlaps cosmid R20004400) to the left from bases 1 to 7,688 of this accession and overlaps cosmid R30064 (AC001107) to the right from bases 33,879 to 45,858. Additional map and sequence information may be obtained at:
http://www-bio.llni.gov/bbrp/genome.html,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACO06123 45858 bp DNA linear PRI 17-DEC-1998
Homo sapiens chromosome 19, cosmid R28177, complete sequence.
ACO06123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

"Lébases 1 to 45858)

Lamerdin, J.E., McCrady, P.M., Skowronski, E., Viswanathan, V.,

Burkhart-Schultz, K., Gordon, L., Dias, J., Kyle, A., Brower, A.,

Stlwagen, S., Phan, H., Velasco, N., Do, L., Regala, W., Terry, A.,

Garnes, J., Danganan, L., Erler, A., Christensen, M., Georgescu, A.,

Avila, J., Liu, S., Attix, C., Andreise, T., Trankheim, M.,

Amico-Keller, G., Coefield, J., Duarte, S., Lucas, S., Bruce, R.,

Thomas, P., Quan, G., Kronmiller, B., Arellano, A., Sanders, C., Cw, D.,

Nolan, M., Trong, S., Kobayashi, A., Olsen, A. S. and Carrano, A.V.
                                                                                                                                                                                                                                                                                                                                                                                                              -----rdcrrrrddacgaddagdcrrrcrcrdddcc 619
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CA 94551, USA
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                                                                                                                                                                                                                                                                                                                                                                                   TrpThrGlyLeuTrpThrGlyLeuGlyGluGlyGluGlyGlyGlyIleGlyProGluGly
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National Laboratory, 7000 East Ave., Livermore,
3 (bases 1 to 45858)
                                                                                                                                                                                          1476
22
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23
7
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  Location/Qualifiers
1. 1476
/ organism="Thermus thermophilus"
//mol type="genomic DNA"
/db_xref="taxon:274"
                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---TrpSerAlaGlyLeuThrValArgAspArgPro 69
                                                                                                                                                                                                                                                                                   Indels:
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                                                                                                                                                                                                                                                                                                                                           US-09-972-032-2 (1-79) x BD179739 (1-1476)
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2 (bases 1 to 45858)
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42.31%
42.31%
21.38%
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Best Local Similarity:
      CDS
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DB:
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AUTHORS
TITLE
JOURNAL
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TITLE
JOURNAL
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LOCUS
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KEYWORDS
SOURCE
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                          FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80456 CGGCCGAGCGCTACCACCGCAGGGTCGCGGACATGCTCGCCACCGGGACGGTCCTGGACG 80397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80336 TCGCCGACGTCTGCCTGGACGCCTCCACCGCGTCGTCCTGGCCGCGCTCGCCCGCGCGC 80277
GTDYIRDDVKDLDTARMLLVGTRGDPATPYRWTTETADRLGPSAVVLDNRGEGHTGYA
SSKCVHRKVDDFLLYGSLPPDGSSCGPESTGDGSG"
complement (5910. . 6809)
                                                                                /note="Pfam match to entry PF00561 abhydrolase, alpha/beta
Mydrolase fold, score 55.00, E-value 1.6e-12"
complement(7217. .7220)
/note="possible RBS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BD179739 1476 bp DNA linear PAT 15-MAY-2003
Highly thermophilic bacterium-derived protein and gene encoding it.
BD179739
                                                                                                                                                                                                                                                                                                                   /note="SC5H1.35c, possible secreted protein, len: 237 aa,
unknown function, probable CDS suggested by positional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene encoding it
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CIZN15/09,C12N15/09,C07K14/195,C12N1/15,C12N1/19,C12N1/21, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C12N9/88,C12P21/02//(C12N9/88,C12R1:01),(C12N15/09,C12R1:01),(C12P21/02,C12R1:01),C12N15/00,C12N15/00,(C12N15/00)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 GlyLeuTrpThrGlyLeuGlyGluGlyGlnGluGlyGlyIleGlyProGluGlyGlnAla 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ပ္ပ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 ArgProArgArgValSerAlaGly------CysGlyPheAlaAspAlaHisTrpThr
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Highly thermophilic bacterium-derived protein and gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80276 TGGTCGACACGCGGCGCGGGGGCGCGCGGGGCGCGGGACCGGCG 80229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 TrpProTrp-----SerAlaGlyLeuThrValArgAspArgPro 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kuramitsu,N. and Yokoyama,S.
Highly thermophilic bacterium-derived protein and genuly patent: JP 2002325574-A. 230 12-NOV-2002;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH
OS Thermus thermophilus
PN JP 2002325574-A/230
PD 12-NOV-2002
PP 12-NOV-2001 JP 2001116171
PI NARMITSU,SHIGSYUKI YOKOYAWA
PC C12N15/09,C12N15/09,C07K14/195,C12N1/15,C12N1/19
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Matches:
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Mismatches:
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JP 2002325574-A/230.
                                                                                                                                                                      437. .7440
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Thermus thermophilus
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Best Local Similarity:
Query Match:
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BD179739
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DEFINITION
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join(<17597. .17713,18795. .18842,20510. .20647,21740. .21801,
24468. .24562,28187. .28272,34238. .34278,34695. .34915,
40091. .40215,43172. .>43480)
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SPGRFRAGVSPLSLSTEARRQASPTLSPLSPLSPLTQAVAMDALSLEQQLDYAFFTQAGS
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2322. . 23455
23407. . 23453
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complement (29671. .29955)
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complement (30288. 30588)
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complement (30590. 30658)
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complement(27004.
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complement (3503. 3799)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="SCI30A.19, unknown, len: 153 aa; similar to many of undefined function e.g. TR:P96807 (EMBL:292770)

Whychetical protein from Mycobacterium tuberculosis (151 aa) fasta scores; opt: 639, z-score: 785.9, E(): 0, (60.8) identity in 148 aa overlap) and SW:NODN RHILLY nodulation protein from Rhizobium leguminosarum (161 aa) fasta scores; opt: 388, z-score: 482.2, E(): 1.6e-19, (44.8% identity in 145 aa overlap)"
                        Submitted (09-MAY-2002) Submitted on behalf of the Streptomyces sequencing team, Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: sdb@sanger.ac.uk on or before Oct 26, 2002 this sequence version replaced gi:20520819, gi:20520889, gi:20520880, gi:20520881, gi:2052081, gi:20520818, gi:20520889, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520018, gi:20520704, gi:20520918, gi:20520704, gi:20520918, gi:20520704, gi:20520704, gi:20520918, gi:20520704, gi:20520918, gi:20520918, gi:20520704, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520704, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, gi:20520918, g
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                                                                                                                                                                                                                                                                                                                                                                                              coelicolor A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="synonym: SCI30A.19"

    .283100
    /organism="Streptomyces/mol_type="genomic DNA"/strain="A3(2)"

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59._.520
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/gene="SC01699"
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            Direct Submission
Submitted (09-MAY-2002)
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Complete ganome sequence of the model actinomycete Streptomyces
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283100 bp DNA linear BCT 11-FBB-Streptomyces coelicolor A3(2) complete genome, segment 7/29.
AL939110 AL035591 AL096743 AL096781 AL096811 AL096839 AL096844 AL096849 AL109848 AL132644 AL445403 AL513407 AL591322 AL645882
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Streptomyces coelicolor A3(2)
Bacteria, Actinobacteria, Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
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Matches:
Conservative:
Mismatches:
Indels:
                            /rpt family="Alur"
32768. 3306
/rpt family="Alur"
3718. 33907
/rpt family="Alur"
complement (37634. 37785)
/rpt family="MRRA"
complement (3787. 38087)
/rpt family="Alusr"
complement (3787. 38281)
/rpt family="Alusr"
/rpt family="Alusr"
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Nature 417 (6885), 141-147 (2002)
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Bentley, S.D.
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97.50
38.38%
32.32%
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Best Local Similarity:
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                                                                                                                                                                                                                                                                         /note="SCI30A.24, possible transcriptional regulator, len: 237aa; similar to many eg. SW:MERR_STRLI probable mercury resistance operon repressor from Streptomyces lividans (125 aa) fasta scores; opt: 144, z-score: 183.3, E(): 0.007, (38.2% identity in 89 aa overlap). Contains Pfam match to entry PP01022 HTH 5, Bacterial regulatory portein, arsR family. Contains possible helix-turn-helix /codon start=1.
                                                                            2925. .3017
/gene="SCO1702"
/note="PS01081 Bacterial regulatory proteins, tetR family
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/note="Pfam match to entry PP00440 tetR, Bacterial regulatory proteins, tetR family, score 45.00, E-value
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protein id="CAB46801.1"
/db_xref="GI:5441777"
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6 4 9
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Matches:
Conservative:
Mismatches:
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AC113007.3 GI:28626712
HTG; HTGS_PHASE1; HTGS_DRAFT.
Mus musculus (house mouse)
Mus musculus
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/gene="SCO1703"
                                                                                                                                                                                                                                         3555. .4268
/gene="SCO1703"
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97.50
33.01%
27.18%
21.38%
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2925.
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KEYWORDS
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complement (1635. 2748)
/gene="SCO1701"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Note="SCI30A.23, possible transcriptional regulator, len: 213 aa, similar to many e.g. TR:Q53901 (BMBL:M64683) equilatory protein from Streptomyces coelifolor (259 aa) fasta scores; opt: 227, z-score: 273.2, E(): 6.9e-08, (32.3% identity in 217 aa overlap). Contains Ffam match to entry PF00440 tetk, Bacterial regulatory proteins, tetk family and Prosite match to PS01081 Bacterial regulatory proteins, tetk family signature. Contains possible helix-turn-helix motif (+5.17 SD) 31-52aa."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /trānslation="warerkdildegetynriveraralydaeglaavstrrlaaelgvsge
slynhfrykdeileavadsvsaqvdlsmfedgrewrtalhdwavsyrtalrdhpnivp
vlahgferrpalhhladavygamvragwpaqatsigalmryfvmgsalgspaggrvd
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2889. 33029
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                                                                                                                                                                                                                                                                                                                                                                                                                            /Jone="SCI30A.22c, probable acyl-CoA dehydrogenase, len:
383 aa; similar to many both prokaryote and eukaryote eg.
SW1ACDB BACSU acyl-CoA dehydrogenase from Bacillus
swbtilis (379 aa) fasta scores; opt: 109,1 z-score:
1197.8, E(): 0, (43.8% identity in 377 aa overlap) and
SW1ACDS RAT acyl-CoA dehydrogenase from Rattus norvegicus
(Rat) (412 aa) fasta scores; opt: 1079, z-score: 1184.2,
B(): 0, (44.6% identity in 372 aa overlap). Contains Pfam
match to entry PF00441 Acyl-CoA_dh, Acyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="pfam match to entry PP00441 Acy1-CoA_dh, Acy1-CoA_dehydrogenase, score 565.20, E-value 4.3e-166."
2850. .3491
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CDS

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NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
      Consensus quality: 191584 bases at least Q20
Insert size: 210000; agarose-fp
Insert size: 192012; sum-of-contigs
Quality coverage: 6.4 in Q20 bases; sum-of-contigs
Quality coverage: 7.0 in Q20 bases; sum-of-contigs
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67687. .72769

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                                                                                                MILE MARCHILIS, CALORE MALES-1499H13

MILE MARCHILIS, CALORE MALES-1499H13

S. (Dazeclauls, CALORE MALES-1499H13

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Center: Whitehead Institute/ MIT Center for Genome Research
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Web site: http://www-seq.wi.mit.edu
                     1 (bases 1 to 193012)
Birren, B., Nusbaum, C. and Lander, E.
Mus musculus, clone RP23-349H13
                     REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
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JOURNAL
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53922 GGCGGCCGCGCATTGTTCTGCGCTGCGGGCGCGTGCGGCGGCCTCGGGTGGCGCTCGG 53863
                                                                                                                                                         46 CysAlaSerArgTrpProArgSerAlaSerArg---TrpProTrpSerAlaGlyLeuThr 64
                                                                 5 proArgArgValSerAlaGlyCysGlyPheAlaAspAlaHisTrpThrGlyLeuTrpThr 24
                                                                                                     ---ProThrProAsp 45
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20
3
Conservative:
Mismatches:
Indels:
Gaps:
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28.72%
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Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-972-032-1
Sequence 1, Application US/09972032
Fublication No. US20020086361A1
Sementa INFORMATION:
APPLICANT: Case Western Reserve University
APPLICANT: Montano, Monica
APPLICANT: Sutton, Amelia
ITLE OF INVENTION: A Modulator of Antiestrogen Pharmacology
FILE REPERENCE: 27708/04003
CURRENT APPLICATION NUMBER: US/09/972,032
CURRENT PILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: US 60/238,190
PRIOR PILING DATE: 2000-10-05
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 990; Conservative 0; Mismatches
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SOFWHARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 990
                                                                       3234
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US-09-972-032-1
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   TYPE: DNA
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Sequence 1095, Ap
Sequence 676, App
Sequence 284, App
Sequence 285, App
Sequence 232, App
Sequence 232, App
Sequence 23812, App
Sequence 1360, App
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1: \( \cgn2 \frac{7}{\text{prodata}} \) / Pubpna/USO7 \text{PUBCOMB.seq:*} \)

2: \( \cgn2 \frac{7}{\text{prodata}} \) / Pubpna/PCT \text{PUB \text{PUB \text{PUB \text{seq:*}}} \)

3: \( \cgn2 \frac{6}{\text{prodata}} \) / Pubpna/USO6 \text{NW \text{PUB \text{seq:*}}} \)

4: \( \cgn2 \frac{6}{\text{prodata}} \) / Pubpna/USO6 \text{NW \text{PUB \text{seq:*}}} \)

5: \( \cgn2 \frac{6}{\text{prodata}} \) / Pubpna/USO6 \text{PUBCOMB.seq:*} \)

6: \( \cgn2 \frac{6}{\text{prodata}} \) / Pubpna/USO8 \text{PUB \text{PUB \text{seq:*}}} \)

7: \( \cgn2 \frac{6}{\text{prodata}} \) / Pubpna/USO8 \text{NW \text{PUB \text{seq:*}}} \)

8: \( \cgn2 \frac{6}{\text{prodata}} \) / Pubpna/USO8 \text{NW \text{PUB \text{seq:*}}} \)

10: \( \cgn2 \frac{6}{\text{prodata}} \) / Pubpna/USO9 \text{PUBCOMB.seq:*} \)

11: \( \cgn2 \frac{6}{\text{prodata}} \) / Pubpna/USO9 \text{NW \text{PUB \text{seq:*}}} \)

12: \( \cgn2 \frac{6}{\text{prodata}} \) / Pubpna/USO9 \text{NW \text{PUB \text{seq:*}}} \)

13: \( \cgn2 \frac{6}{\text{prodata}} \) / Pubpna/USO9 \text{NW \text{PUB \text{seq:*}}} \)

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17: \( \cgn2 \frac{6}{\text{prodata}} \) / Pubpna/USO9 \text{NW \text{PUB \text{seq:*}}} \)

18: \( \cgn2 \frac{6}{\text{prodata}} \) / Pubpna/USO0 \text{NW \text{PUB \text{seq:*}}} \)

19: \( \cgn2 \frac{6}{\text{prodata}} \) / Pubpna/USO0 \text{NW \text{PUB \text{seq:*}}} \)

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19: \( \cgn2 \frac{6}{\text{prodata}} \) / Pubpna/USO0 \text{NW \text{PUB \text{seq:*}}} \)
                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-764-891-1098

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US-09-873-3670-285

US-09-86-0078-232

US-10-087-192-1360

US-10-027-632-23812

US-10-027-632-167845

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Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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Post-proces: Database :

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Sequence:

CCTCAGCTTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCGCGCCCGGCCCCCGACAC 120

CTAGITITTAAAGGGCCCCTGCTGITGCTGCTGCCGCCGCCGCTCCCCAGCTGCCCAGTCTG CTAGTTTTTAAAGGGCCCCTGCTGTTTGCTGCCGCCGCCGCCGCTCCCAGCTGCCAGTCTG

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Result No.

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US-09-764-891-1098
                                                                                          or
                                                                                                                                               or
                                                 NAME/KEY: SITE
LOCATION: (358)
OTHER INFORMATION: n equals a,t,g, o. NAME/KEY: SITE
LOCATION: (378)
OTHER INFORMATION: n equals a,t,g, o. NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 676, Application US/10087192; Publication No. US20020182586A1; GENERAL INFORMATION:
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US-10-087-192-148/c
'Sequence 148, Application US/10087192
'Publication No. US2020182586A1
'CENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  932 AATTGCAAGATCTGTGGTGC 951
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US-10-087-192-676
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                                                                                                                                                                                                                                                                                         80; Conservative
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LOCATION: (1)...(114619
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TYPE: DNA ORGANISM:
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Best Local S
Matches 55
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                                            GCGGCTCAGTCCCGCGTTGCCATGTGTGGGAGACCGCGTCGCGTAAGCGCTGGATGTGG
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                                                                                                                 CTTCGCTGATGCACATTGGACCCGGGCTCTGGACTGGGCTAGGGGGAAGGCAAGAGGGCGGG 300
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| Sequence 1098, Application US/09764891
| Publication No. US20030077808A1
| Publication No. US20030077808A1
| APPLICANT: Rosen et al. |
| TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
| TURENT APPLICATION NUMBER: US/09/764,891
| CURRENT APPLICATION NUMBER: US/09/764,891
| CURRENT APPLICATION NUMBER: US/09/764,891
| Prior application data removed - consult PALM or file wrapper
| NUMBER OF SEQ ID NOS: 10231
| SEQ ID NO 1098
| LENGTH: 404
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  Length 404;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: BORGELHAIG W.
APPLICANT: BRIGHLAIG, DAVIG W.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: OANCER
FILE REFERENCE: 529452000122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
FRICR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
FRICR FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: PRACE TO NOS: 2059
SOFTWARE: PRACE OF WINDOWS Version 4.0
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APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER
                            3.3e-30;
8.1%; Score 80; DB 10;
100.0%; Pred. No. 3.3e-30;
iive 0; Mismatches 0;
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ORGANISM: Homo sapiens
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Matches 51; Conserv
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APPLICANT: Soppet, Daniel
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APPLICANT: Soppet, Daniel
APPLICANT: Endress, Gregory
APPLICANT: Augustus, Meena
APPLICANT: Endress, Gregory
APPLICANT: Endres, Meena
APPLICANT: Carter, Kenneth
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
TITLE OF INVENTION: Signature Gene Sets
FILE REFERENCE: 689290-64
CURRENT APPLICATION NUMBER: US. 60/236,891
PRIOR APPLICATION NUMBER: U.S. 60/236,842
PRIOR PILING DATE: 2000-09-29
PRIOR PELING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: U.S. 60/244,867
PRIOR APPLICATION NUMBER: U.S. 60/244,867
PRIOR APPLICATION NUMBER: U.S. 60/244,867
PRIOR PILING DATE: 2000-11-01
PRIOR PILING DATE: 2000-11-01
PRIOR RILING DATE: 2000-11-01
PRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 2000-11-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 5.5%; Score 54; DB 13; Length 174448; Best Local Similarity 100.0%; Pred. No. 2.6e-17; Matches 54; Conservative 0; Mismatches 0; Indels 0;
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CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 148
LENGTH: 174448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-873-367C-285; Sequence 285, Application US/09873367C; Publication No. US20030165839A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 284, Application US/09873367C; Publication No. US20030165839A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1)...(174448)
, CTHER INFORMATION: n = A,T,C or G
US-10-087-192-148
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SOFTWARE: PatentIn version 3.0
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US-09-873-367C-284
                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Young, Paul
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LENGTH: 149480
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GENERAL INFORMATION:

APPLICANT: EDNer, Reinhard

APPLICANT: EDNer, Reinhard

APPLICANT: EDNer, Reinhard

TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Usining Sign.

TITLE OF INVENTION: Gene Sets

TITLE OF INVENTION: Gene Sets

TITLE OF INVENTION: Gene Sets

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TITLE OF INVENTION: Gene Sets

CURRENT FILING DATE: 2000-10-02

PRIOR FILING DATE: 2000-10-02

PRIOR APPLICATION NUMBER: US/60/237,278

PRIOR PELING DATE: 2000-10-02

PRIOR FILING DATE: 2000-10-02

PRIOR FILING DATE: 2000-10-02

PRIOR PELING DATE: 2000-10-02

PRIOR APPLICATION NUMBER: US/60/237,294

PRIOR APPLICATION NUMBER: US/60/237,295

PRIOR APPLICATION NUMBER: US/60/237,316

PRIOR APPLICATION NUMBER: US/60/237,316

PRIOR APPLICATION NUMBER: US/60/237,316

PRIOR APPLICATION NUMBER: US/60/237,316

PRIOR APPLICATION NUMBER: US/60/237,316

PRIOR APPLICATION NUMBER: US/60/237,316

PRIOR APPLICATION NUMBER: US/60/237,316
                                                              APPLICANT: Augustus, Meena
APPLICANT: Buner, Reinhard
APPLICANT: Ebner, Reinhard
APPLICANT: Ebner, Reinhard
APPLICANT: Carter, Aennard
APPLICANT: Carter, Aennard
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
TITLE OF INVENTION: Signature Gene Sets
TITLE OF INVENTION: Signature Gene Sets
FILIE REFERENCE: 689290-64
CURRENT APPLICATION NUMBER: US/09/873,367C
CURRENT FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: U.S. 60/236,842
PRIOR PILING DATE: 2000-11-01
PRIOR PILING DATE: 2000-11-01
PRIOR FILING DATE: 2000-11-01
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5.2%; Score 51; DB 12; Length 149480;
Best Local Similarity 100.0%; Pred. No. 8.8e-16;
Matches 51; Conservative 0; Mismatches 0; Indels 0;
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Pred, No. 8.8e-16;
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Soppet, Daniel
Endress, Gregory
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US-09-968-007A-232
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Best Local Similarity
Matches 49; Conserv
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4.9%; Score 49; DB 13; Length 738;
Best Local Similarity 100.0%; Pred. No. 1.8e-14;
Matches 49; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 2.7e-15;
Matches 50; Conservative 0; Mismatches 0; Indels
                                                  TYPE: DNA
ORGANISM: Homo sapiens
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                                  RESULT 8
US-10-087-192-1360
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US-10-087-192-1360
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SOFTWARE: FASCSE
SEQ ID NO 23812
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RESULT 10
US-10-027-633-23812
; Sequence 23812, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT PEPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR PAPLICATION NUMBER: US 60/218,006
PRIOR PAPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-04-20
PRIOR PLING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
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PRIOR STRING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR STRING DATE: 1999-09-28
PRIOR STRING DATE: 1999-09-28
PRIOR SEQ ID NOS: 325720
SOFTWARE: PASEESO for Windows Version 4.0
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| Sequence 167845, Application US/10027632
| Sequence 167845, Application US/10027632
| Publication No. US2020198371A1
| GENERAL INFORMATION: Identification and Mapping of Single Nucleotide | TITLE OF INVENTION: Pelymorphisms in the Human Genome | TITLE OF INVENTION: Pelymorphisms in the Human Genome | TITLE OF INVENTION: Polymorphisms in the Human Genome | TITLE OF INVENTION: 10827.129
| CURRENT APPLICATION NUMBER: US/10/027,632 | CURRENT FILING DATE: 2002-04-30 | PRIOR APPLICATION NUMBER: US 60/188,006 | PRIOR APPLICATION NUMBER: US 60/198,676 | PRIOR PELING DATE: 2000-07-12 | PRIOR PELING DATE: 2000-04-20 | PRIOR PELING DATE: 2000-04-20 | PRIOR PELING DATE: 2000-03-29 | PRIOR APPLICATION NUMBER: US 60/198,218 | PRIOR APPLICATION NUMBER: US 60/165,363 | PRIOR APPLICATION NUMBER: US 60/165,363 | PRIOR APPLICATION NUMBER: US 60/156,363 | PRIOR PILING DATE: 1999-11-23 | PRIOR APPLICATION NUMBER: US 60/166,368 | PRIOR APPLICATION NUMBER: US 60/166,002 | PRIOR APPLICATION NUMBER: US 60/166,002 | PRIOR APPLICATION NUMBER: US 60/166,002 | PRIOR APPLICATION NUMBER: US 60/166,002 | PRIOR APPLICATION NUMBER: US 60/166,002 | PRIOR APPLICATION NUMBER: US 60/166,002 | PRIOR APPLICATION NUMBER: US 60/166,002 | PRIOR APPLICATION NUMBER: US 60/166,002 | PRIOR APPLICATION NUMBER: US 60/166,002 | PRIOR APPLICATION NUMBER: US 60/166,002 | PRIOR APPLICATION NUMBER: US 60/166,002 | PRIOR APPLICATION NUMBER: US 60/166,002 | PRIOR APPLICATION NUMBER: US 60/166,002 | PRIOR APPLICATION NUMBER: US 60/166,002 | PRIOR APPLICATION NUMBER: US 60/166,002 | PRIOR APPLICATION NUMBER: US 60/166,002 | PRIOR APPLICATION NUMBER: US 60/166,002 | PRIOR APPLICATION NUMBER: US 60/166,002 | PRIOR APPLICATION NUMBER: US 60/166,002 | PRIOR APPLICATION NUMBER: US 60/166,002 | PRIOR APPLICATION NUMBER: US 60/166,002 | PRIOR APPLICATION NUMBER: US 60/166,002 | PRIOR APPLICATION NUMBER: US 60/166,002 | PRIOR APPLICATION UMBER: US 60/166,002 | PRIOR APPLICATION UMBER: US 60/166,002 | PRIOR APPLICATION UMBER: US 60/166,002 | PRIOR APP
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34 CGATCTCCTGACCTCGTGATCCGCCCCCCCTCAGCTTCCCAAAGTGCTGG
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PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PLING DATE: 2000-03-29
PRIOR FLING DATE: 2000-02-24
PRIOR FLING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-38
PRIOR PLING DATE: 1999-09-38
PRIOR PLING DATE: 1999-09-38
PRIOR PLING DATE: 1999-09-39
PRIOR PLING DATE: 1999-09-09
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US-10-027-632-167846/c
; Sequence 167846, Application US/10027632
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Matches 49; Conserv
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GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER:
US 60/218,006
PRIOR PILITATION NUMBER:
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US 60/218,006
PRIOR FILING DATE:
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                                                                                                                                                                                                                                                                    4.9%; Score 49; DB 13;
llarity 100.0%; Pred. No. 1.8e-14
Conservative 0; Mismatches 0
          NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 167845
LENGTH: 827
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Best Local Similarity
Matches 49; Conserv
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US-10-027-632-167847/c
                                                                                                                                   ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-167845
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US-10-027-632-167845/C

| Sequence 167845, Application US/10027632
| Publication No. US2030204075A9
| Publication No. US2030204075A9
| GENERAL INFORMATION:
| APPLICANT WARGE | David G. | | |
| TTLE OF INVENTION: Delymorphisms in the Human Genome | TTLE OF INVENTION: Polymorphisms in the Human Genome | TTLE OF INVENTION: POLYMORPHISMS in the Human Genome | TTLE REFERENCE: 108827.129 |
| CURRENT APPLICATION NUMBER: US 60/218,006 | PRIOR FILING DATE: 2002-04-30 | PRIOR FILING DATE: 2000-07-12 |
| PRIOR FILING DATE: 2000-07-20 | PRIOR APPLICATION NUMBER: US 60/199,483 |
| PRIOR FILING DATE: 2000-04-20 | PRIOR APPLICATION NUMBER: US 60/185,218 |
| PRIOR FILING DATE: 2000-03-29 | PRIOR FILING DATE: 1999-11-23 |
| PRIOR FILING DATE: 1999-11-23 | PRIOR APPLICATION NUMBER: US 60/186,358 |
| PRIOR FILING DATE: 1999-08-08 | PRIOR PILING DATE: 1999-08-08 |
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4.9%; Score 49; DB 13; Length 827; 00.0%; Pred. No. 1.8e-14;
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Publication No. US20030204075A9;
GEMERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT PELING DATE: 2002-04.30
PRIOR PILING DATE: 2000-07-12
PRIOR PLING DATE: 2000-07-12
PRIOR PLING DATE: 2000-07-20
PRIOR PLING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FEATSEQ for Windows Version 4.0
SEQ ID NO 167846
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ORGANISM: Human
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Search completed: July 10, 2004, 16:51:03 Job time : 544 secs

704 GCCGCCTCAGCTTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCGC 656

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2 1/USFO spool/V09972032/runat 06072004_121534_8872/app_query.fasta_1.263
-Q=/cgn2 1/USFO spool/V09972032/runat 06072004_120534_8872/app_query.fasta_1.263
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=0.1go -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE-LOCAL -OUTFMT=pto
-NORM=ext -HBRASIZE=500 -MNINEN=0 -MAXLENS=2000000000
-NORM=ext -HBRASIZE=500 -MNINEN=0 -MAXLENS=2000000000
-NORM=ext -NORM=CART -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DBLOP=6 -DBLORT=7
                                                                                                                                                                                                       July 10, 2004, 18:59:03; Search time 2822 Seconds (without alignments) 1213.359 Million cell updates/sec
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79
1 MCGRPRRVSAGCGFADAHWT......SAGLTVRDRPQLGELCMGRG 79
                                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                OM protein - nucleic search, using frame_plus_p2n model
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Perfect score:
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SOURCE

REFERENCE AUTHORS TITLE

JOURNAL REFERENCE AUTHORS TITLE JOURNAL

COMMENT

LOCUS DEFINITION

AC073869

ACCESSION

VERSION KEYWORDS

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AC135044 195476 bp DNA linear HTG 05-OCT-2002 Homo sapiens chromosome 16 clone CTD-2551B20, WORKING DRAFT SEQUENCE, 22 unordered pieces.
                                                                                                                                                                                                           Direct Submission
Submitted (05-0CT-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA -----Genome Center
Center Code: Joint Genome Institute
Center Code: Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Consensus quality: 171229 bases at least Q40
Consensus quality: 18238 bases at least Q30
Consensus quality: 188095 bases at least Q30
Consensus quality: 188095 bases at least Q30
Estimated insert size: 193376; sum-of-contigs estimation
Cuality coverage: 7.63 in Q20 bases; agarose-fp estimation
Quality coverage: 6.7 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
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* arbitrary. Gaps between the contigs are represented as
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* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                    Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases I to 195476)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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1302: gap of unknown length
2468: contig of 1166 bp in length
2568: gap of unknow
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AC135044.1 GI:23505535
HTG; HTGS_PHASE1; HTGS_BRAFT; HTGS_ACTIVEFIN.
Homo sapiens (human)
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DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
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DOE Joint Genome Institute.
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2 (bases 1 to 195476)
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DB:
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               DNA linear HTG 05-OCT-2002 CTD-2551B20, WORKING DRAFT
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Direct Submission
Submitted (05-00T-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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Consensus quality: 182638 bases at least Q30
Consensus quality: 188058 bases at least Q30
Consensus quality: 188095 bases at least Q30
Estimated insert size: 193376; sum-of-contigs estimation
Quality coverage: 7.63 in Q20 bases; sum-of-contigs estimation
Quality coverage: 6.7 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a "working draft" sequence. It currently
* consists of 22 contigs. The true order of the pieces
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* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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10 (bases 1 to 195476)
10 Joint Genome Institute.
Sequencing of Human Chromosome 16
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1302: gap of unknown length
2468: contig of 1166 bp in length
2568: gap of unknow
                                                                                                       AC135044.1 GI:23505535
HTG: HTGS PHASB1; HTGS_DRAFT; HTGS_ACTIVEFIN.
Homo sapiens (human)
Homo sapiens
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ACISSO41.1 GI:23SOSS3S
HTG; HTGS PHASEL; HTGS_DRAFT; HTGS_ACTIVEFIN.
HOme sapiens (human)
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Matches:
Conservative:
Mismatches:
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Center clone name: CITB-E1_2551B20
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               195476 bp
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Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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                                      Homo sapiens chromosome 16 clo
SEQUENCE, 22 unordered pieces.
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Query Match: DB:

DEFINITION

AC135044 LOCUS RESULT 2

g 8

ACCESSION VERSION KEYWORDS SOURCE

Best Local

Pred. No.:

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Consensus quality: 171229 bases at least Q40
Consensus quality: 182638 bases at least Q30
Consensus quality: 182638 bases at least Q30
Consensus quality: 188095 bases at least Q30
Consensus quality: 188095 bases at least Q30
Estimated insert size: 1700000; agarose-fp estimation
Batimated insert size: 1700000; agarose-fp estimation
Quality coverage: 7.63 in Q20 bases; sum-of-contigs estimation

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* arbitrary. Gaps between the contigs are represented as

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* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
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                                                                Center clone name: CITB-E1_2551B20
                   Project Information
Center Project Name: 809609
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AC135044
AC135044.1 G1:2350535
HTG; HTGS PHARE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
Homo sapiens (human)
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Consensus quality: 18238 bases at least 020
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Consensus quality: 188038 bases at least 020
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Quality coverage: 7.63 in 020 bases; agarose-fp estimation

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* as soon as it is available and the accession number will

* be preserved.
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DOE Joint Genome Institute.
Direct Submission
Submitted (05-007-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA -----Genome Center
Center: Joint Genome Institute
Center: Joint Genome Institute
Center Code: JGI
Web Site: http://www.jgi.doe.gov
  DOE Joint Genome Institute.

Direct Submission
Submitted (05-072-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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1 (bases 1 to 195476)

DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
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Matches:
Conservative:
Mismatches:
Indels:
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Center clone name: CITB-E1_2551B20
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Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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Home sapiens chromosome 165476 bp DNA linear HTG 05-OCT-2002 SEQUENCE, 22 unordered pieces.
AC135044
AC135044.1 GI:2350535
HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
Home sapiens (human)
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Direct Submission Institute.
Direct Submission Sequencing Facility, DOE Joint Sedonne Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA Center: Joint Genome Institute.
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1 (bases 1 to 195476)

DOB Joint Genome Institute.

Sequencing of Human Chromosome 16

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Consensus quality: 171229 bases at least Q40
Consensus quality: 182638 bases at least Q30
    Length:
Matches:
Conservative:
Mismatches:
Indels:
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Center clone name: CITB-E1_2551B20
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Query Match:
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Consensus quality: 188095 bases at least Q20
Estimated insert size: 170000; agarose-fp estimation
Estimated insert size: 130376; sum-of-contigs estimation
Quality coverage: 7.63 in Q20 bases; agarose-fp estimation
Quality coverage: 6.7 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 22 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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Homo sapiens chromosome 16 clone CTD-2551B20, WORKING DRAFT
SEQUENCE, 22 unordered pieces.
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Submitted (05-OCT-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Malnut Creek, CA 94598, USA
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Catarrhini, Hominidae, Homo.
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Consensus quality: 186538 bases at least Q30
Consensus quality: 188095 bases at least Q30
Estimated insert size: 170000; agarose-fp estimation
Estimated insert size: 193376; sum-of-configs estimation
Quality coverage: 6.7 in Q20 bases; agarose-fp estimation
Quality coverage: 6.7 in Q20 bases; sum-of-configs estimation
* NOTE: This is a "working draft' sequence. It currently
* consists of 22 configs. The true order of the pieces
* is not known and their order in this sequence record is
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1302: gap of unknown length
2468: contig of 1166 bp in length
2568: gap of unknow
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Center clone name: CITB-E1_2551B20
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Center: Joint Genome Institute
Center Code: JGI
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Mammalia; Eutheria; Primates;
I Chases I to 195476)
DOE Joint Genome Institute.
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AC135044 195476 bp DNA linear HTG 05-OCT-2002 Homo sapiens chromosome 16 clone CTD-2551B20, WORKING DRAFT SEQUENCE, 22 unordered pieces.
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Consensus quality: 18238 bases at least Q30
Consensus quality: 188035 bases at least Q30
Consensus quality: 188095 bases at least Q30
Estimated insert size: 193376; sum-of-contigs estimation
Estimated insert size: 193376; sum-of-contigs estimation
Quality coverage: 7.63 in Q20 bases; agneose-fp estimation.
* NOTE: This is a 'working draft' sequence. It currently
consists of 22 contigs. The true order of the pleces
* is not known and their order in this sequence record is
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* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Submitted (05-OCT-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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1 (bases 1 to 1954/6)
DOE Joint Genome Institute.
arbitrary, Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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1302: gap of unknown length
2468: contig of 1166 bp in length
2568: gap of unknow
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ACI35044.1 GI:23505535
HTG; HTGS_PHASE1, HTGS_DRAFT; HTGS_ACTIVEFIN.
Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Bukaryota; Marazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Consensus quality: 171229 bases at least 040
Consensus quality: 182638 bases at least 030
Consensus quality: 182638 bases at least 020
Estimated insert size: 170000; agarose-fp estimation
Estimated insert size: 13376; sum-of-contigs estimation
Quality coverage: 7.63 in 020 bases; agarose-fp estimation

* NOTE: This is a 'working draft' sequence. It currently

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* be preserved.
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Center Project Name: 808609
Center clone name: CITB-E1_2551B20
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Consensus quality: 171229 bases at least Q40
Consensus quality: 182638 bases at least Q20
Consensus quality: 182638 bases at least Q20
Consensus quality: 182695 bases at least Q20
Estimated insert size: 170000; agarose-fp estimation
Estimated insert size: 19376; sum-of-contigs estimation
Quality coverage: 7.63 in Q20 bases; agarose-fp estimation
* NOTE: This is a 'working draft' sequence. It currently
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* as soon as it is available and the accession number will
* be preserved.
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DOE Joint Genome Institute.
DOE Joint Genome Institute.
DIECT Submission
Submitted (05-007-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Center: Joint Genome Institute
Center Joint Genome Institute
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HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
HTGS: HTGS_DHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
HTGMO Sapiens
HOMO Sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
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1302: gap of unknown length
2468: contig of 1166 bp in length
2568: gap of unknow
                                                                                    Length:
Matches:
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Mismatches:
Indels:
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Center clone name: CITB-E1_2551B20
   2568: gap of unknow
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Best Local Similarity:
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AUTHORS
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AC135044
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195476 5 0 0

Length:
Matches:
Conservative:
Mismatches:
Indels:

1.04e+03 9.00 100.00% 100.00%

Percent Similarity: Best Local Similarity: Query Match:

Pred. No.:

VERSION KEYWORDS SOURCE ORGANISM

JOURNAL REFERENCE AUTHORS TITLE JOURNAL

COMMENT

REFERENCE AUTHORS TITLE

DEFINITION

ACCESSION

RESULT 10 AC135044 LOCUS

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AC135044 195476 bp DNA linear HTG 05-OCT-2002 Homo sapiens chromosome 16 clone CTD-2551B20, WORKING DRAFT SEQUENCE, 22 unordered pieces.
                                                                                                                                                                                                                              Direct Submission.

Submitted (05-0CT-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA Center: Joint Genome Institute
Center: Joint Genome Institute
Center Code: JGI
                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 195476)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Consensus quality: 171229 bases at least Q40
Consensus quality: 182638 bases at least Q30
Consensus quality: 188055 bases at least Q30
Consensus quality: 188055 bases at least Q20
Estimated insert size: 17080; agarose-fp estimation
Estimated insert size: 193376; sum-of-contigs estimation
Quality coverage: 7.63 in Q20 bases; agarose-fp estimation

* NOTE: This is a * working draft' sequence. It currently

* consists of 22 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
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1302: gap of unknown length
2468: contig of 1166 bp in length
2568: gap of unknow
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Homo sapiens (human)
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Center Project Name: 809609
Center clone name: CITB-E1_2551B20
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Sequencing of Human Chromosome 16
Unpublished
2 [Dases 1 to 195476]
DOE Joint Genome Institute.
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AC135044.1 GI:23505535
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Homo sapiens (human)
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AC135044/c
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                            AC135044 195476 bp DNA linear HTG 05-OCT-2002 Homo sapiens chromosome 16 clone CTD-2551B20, WORKING DRAFT SEQUENCE, 22 unordered pieces.
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AC135044.1 GI:23505535
HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
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Consensus quality: 18638 bases at least Q30
Consensus quality: 186095 bases at least Q20
Estimated insert size: 170000; agarose-fp estimation
Estimated insert size: 170000; agarose-fp estimation
Quality coverage: 7.63 in Q20 bases; sum-of-contigs estimation
Quality coverage: 6.7 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a "working draft" sequence. It currently
* consists of 22 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N. but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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DDB Joint Genome Institute.
Direct Submission
Submitted (05-0CT-2002) Production Sequencing Facility, DOB Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA Center: Joint Genome Institute
Center: Joint Genome Institute
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gap of unknown length
contig of 1166 bp in length
gap of unknow
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HTG; HTGS_PHASB1; HTGS_DRAFT; HTGS_ACTIVEFIN.
Homo sapiens (human)
Homo sapiens
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Center Project Name: 809609
Center clone name: CITB-B1_2551B20
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Unpublished
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LOCUS

RESULT 11 AC135044 ACCESSION VERSION KEYWORDS

Query Match

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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AC135044
Homo sapiens chromosome 16 clone CTD-2551B20, WORKING DRAFT
SEQUENCE, 22 unordered pieces.

MC135044.1 GI:23505535
AC135044.1 GI:23505535
HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
Homo sapiens (human)
ESM Homo sapiens (human)
Homo sapiens (human)
Homo sapiens (human)

ESM Homo sapiens (hordata; Craniata; Vertebrata; Euteleostomi;
Homo sapiens (human)

ESM Homo sapiens (hordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 195476)
ES Guenoing of Human Chromosome 16
Unpublished
Dob Joint Genome Institute.

Stabension
Submitted (05-0CT-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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Center: Joint Genome Institute
Center: Joint Genome Institute
Center: Joint Genome Institute
Center: Joint Genome Institute
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Consensus quality: 171229 bases at least 040
Consensus quality: 18638 bases at least 030
Consensus quality: 18638 bases at least 020
Estimated insert size: 170006; agarose-fp estimation
Estimated insert size: 170006; agarose-fp estimation
Quality coverage: 7.63 in 020 bases; sum-of-contigs estimation
Quality coverage: 6.7 in 020 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 22 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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1302: gap of unknown length
2468: contig of 1166 bp in length
2568: gap of unknow
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Consensus quality: 171229 bases at least
                                                   Project Information
Center Project Name: 809609
Center clone name: CITB-E1_2551B20
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Center clone name: CITB-E1_2551B20
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VERSION
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AC135044/c
LOCUS
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AUTHORS
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AC135044
AC135044.1 GI:23505535
HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
Homo sapiens (human)
Eukarvar.
2 (bases 1 to 195476)
DOB Joint Genome Institute.
Direct Submission
Submisted (05-007-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94596, USA Center: Joint Genome Institute
Center: Joint Genome Institute
Center Code: JGI Genome JGI Goe.gov
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Consensus quality: 182638 bases at least Q30
Consensus quality: 188058 bases at least Q30
Consensus quality: 188095 bases at least Q30
Consensus quality: 188095 bases at least Q30
Estimated insert size: 170000; agarose-fp estimation
Quality coverage: 7.63 in Q20 bases; agarose-fp estimation
Quality coverage: 6.7 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 22 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* trus of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 195476)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
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1302: gap of unknown length
2468: contig of 1166 bp in length
2568: gap of unknow
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Matches:
Conservative:
Mismatches:
Indels:
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Center Project Name: 809609
Center clone name: CITB-E1_2551B20
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2 (bases 1 to 195476)
DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                 Summary Statistics
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Best Local Similarity:
Query Match:
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Pred. No.:

RESULT 13 AC135044/c LOCUS

8

DEFINITION

ACCESSION

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

us-09-972-032-2.rge

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Search completed: July 10, 2004, 20:57:09 Job time : 3260 secs
                                                                                                                                                                                                                                                                 Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                               Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC135044 195476 bp DNA linear HTG 05-OCT-2002 Homo sapiens chromosome 16 clone CTD-2551B20, WORKING DRAFT SEQUENCE, 22 unordered pieces.
Consensus quality: 182638 bases at least Q30
Consensus quality: 188095 bases at least Q20
Estimated insert size: 170000; agarose-fp estimation
Estimated insert size: 170000; agarose-fp estimation
Quality coverage: 7.63 in Q20 bases; sum-of-contigs estimation
Quality coverage: 6.7 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 22 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* truns of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (05-OCT-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
----Genome Center
Center: Joint Genome Institute
Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata, Vertebrata; Buteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Consensus quality: 171229 bases at least Q40
Consensus quality: 182638 bases at least Q30
Consensus quality: 188695 bases at least Q30
Consensus quality: 188095 bases at least Q30
Estimated insert size: 170000; agarose-fp estimation
Quality coverage: 7.63 in Q20 bases; agarose-fp estimation
Quality coverage: 6.7 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 22 contigs. The true order of the pieces
                                                                                                                                                                                                                                                                                                                              contig of 1202 bp in length
gap of unknown length
contig of 1166 bp in length
gap of unknow
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ACI35044.1 GI:23505535
HTGS_HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
Homo sapiens (human)
Homo sapiens
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Matches:
Conservative:
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Center Project Name: 809609
Center clone name: CITB-E1_2551B20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (1-195476)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
1 (bases 1 to 195476)
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DOE Joint Genome Institute.
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KEYWORDS
SOURCE
ORGANISM
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AC135044
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TITLE
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AUTHORS
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JOURNAL
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* arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
not known and their order in this sequence record is
                                                                                                                                    1202: contig of 1202 bp in length
1302: gap of unknown length
2468: contig of 1166 bp in length
2568: gap of unknow
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Mismatches:
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100.00%
11.39%
                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
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, Xgapext 60.0 , Ygapext 60.0 , Fgapext 7.0 , Delext 7.0

OLIGO Xgapop 60.0 , Ygapop 60.0 , Fgapop 6.0 , Delop 6.0 ,

score:

Title: Perfect :

Sequence:

Scoring table:

July 12, 2004, 19:22:20

ı

OM protein

Run on:

Post-processing: Listing first 45 summaries

Database

Query. Match Length DB

Score

Result No.

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Word size:

Searched:

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Sequence 7577, Ap. Sequence 23591, Ap. Sequence 2075, Ap. Sequence 20103, A Sequence 19, Appl. Sequence 19, Appl. Sequence 19, Appl. Sequence 1015, Appl. Sequence 1015, Appl. Sequence 1015, Appl. Sequence 1115, Appl. Se
                                                     Sequence 31286, Ap Sequence 1599, Ap Sequence 11225, A Sequence 11766, A Sequence 37767, A Sequence 37767, A Sequence 37767, A Sequence 13444, A Sequence 7, Appli Sequence 5, Appli Sequence 5, Appli Sequence 33317, A Sequence 5, Appli Sequence 35317, A Sequence 5, Appli Sequence 35317, A Sequence 5, Appli
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38332, A
35061, A
8, Appli
34535, A
885, App
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92083, A
54, Appl
190, App
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Sequence
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| Publication No. US20020086361A1
| GENERAL INFORMATION:
| APPLICANT: Case Western Reserve University
| APPLICANT: Montano, Monica |
| APPLICANT: Montano, Monica |
| APPLICANT: Montano, Monica |
| APPLICANT: Montano, Maelia |
| TITLE OF INVENTION: A Modulator of Antiestrogen Pharmacology |
| FILE REFERENCE: 27708/04003 |
| CURRENT APPLICATION NUMBER: US/09/972,032 |
| CURRENT FILING DATE: 2001-10-05 |
| PRIOR APPLICANTION NUMBER: US 60/238,190 |
| PRIOR APPLICANTION NUMBER: US 60/238,190 |
| NUMBER OF SEQ ID NOS: 2 |
| SOFTWARE: Patentin version 3.1
                                               2 US-10-43128

2 US-10-43128

3 US-10-232-1599

5 US-10-282-1599

6 US-10-282-122A-11225

6 US-10-289-493-35593

6 US-10-289-493-35593

7 US-10-425-114-13161

3 US-10-425-114-13161

3 US-10-282-122A-13867

5 US-10-282-122A-13867

5 US-10-282-122A-13867

5 US-10-282-122A-13867

8 US-10-282-122A-13867

9 US-10-425-114-20795

3 US-10-425-114-20795

3 US-10-425-114-20795

4 US-10-425-114-20795

5 US-10-61-902-19

6 US-10-61-902-19

6 US-10-61-902-19

7 US-10-425-114-3206

8 US-10-61-902-19

9 US-10-61-902-19

10-156-761-1015

6 US-10-61-902-19

10-10-425-114-35061

3 US-10-132-350-19

6 US-10-156-761-1015

6 US-10-156-761-1015

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6 US-10-156-761-1015

7 US-10-152-114-35061

3 US-10-152-114-35061

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5 US-10-200-521-190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Homo sapiens
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LENGIH: 990
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US-09-972-032-1
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-MODEL=frame+ p2n model - DEV=x1h
-Q-Cgn2 1/USFTO_spool/US09972032/runat_06072004_121537_8984/app_query.fasta_1.263
-Q-Cgn2 1/USFTO_spool/US09972032/runat_06072004_121537_8984/app_query.fasta_1.263
-QB-Published Applications NA -QFWT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNIT$=bits -START=1 -RND=1 -MATRIX=01igo
-TRANS=humand+0.cdi -LISTAS=5 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
-ALIGN=15 -MODE=LOCAL -OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09972032_@CGN 1 1511_@runat_06072004_121537_8984
-NOPUS=6 -ICPUS=1 - NORMAP - LARGORDUSEX - NEG_SCORE=0 - WAIT - DSPBLOCK=100
-LONGLOG -DEV_TINEOUT=120 -WARN TINEOUT=30 -TEREADS=1 -KGAPOP=60 -KGAPEXT=60
-FGAPOP=6 -FGĀPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELOP=6 -DELOP=7
                                                                                                                                                                                                               (without alignments)
965.004 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                 US-09-972-032-2
79
1 MCGRPRRVSAGCGFADAHWI.....SAGLITVRDRPQLGELCWGRG 79
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| cgn2_6/ptodata/2/pubpna/USO7 PUBCONB.seq:*
| cgn2_6/ptodata/2/pubpna/DC7 NEW PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6 NEW PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6 NEW PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_NEW PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_NEW PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO8 NEW PUB.seq:*
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| cgn2_6/ptodata/2/pubpna/USO8_PUBCONB.seq:*
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| cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO8_PUBCONB.seq:*
| cgn2_6/ptodata/2/pubpna/USO8_PUBCONB.seq:*
| cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
                                                                                                                                                                                ; Search time 399 Seconds
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   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                 nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3183909 segs, 2436941669 residues
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4452379 TCGCGCTGGCCGAGAAGTGCATCGCGTTGGCCA 4452411

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Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                         203 ATGTGTGGGAAGACCGCGTCGCGTAAGCGCTGGATGTGGCTTCGCTGATGCACATTGGACC 262
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                                                                                                                                                                                                                                                                                                                            1 MetCysGlyArgProArgArgValSerAlaGlyCysGlyPheAlaAspAlaHisTrpThr 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 GCAGGTCTTACCGTCCGAGATCGTCCGCAACTGGGCGAGCTGTGCATGGGGCGTGGC 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AlaGlyLeuThrValArgAspArgProGlnLeuGlyGluLeuCysMetGlyArgGly 79
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Conservative:
Mismatches:
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LOCATION: (4187715)
OTHER INFORMATION: a, t, c, g, other or unknown
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APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIKAWA, JUN
APPLICANT: SHIRAW, JUN
APPLICANT: SATEMI YOSHIYUKI
APPLICANT: SATAKI YOSHIYUKI
APPLICANT: AATTORI, MASAHIRA
TITLE OF INVENITON: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-26
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT PLILING DATE: 2002-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR RPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-06-02
NUMBER OF SEQ ID NOS: 15109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 1, Application US/10156761; Publication No. US20030119018A1; GENERAL INFORMATION:
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Best Local Similarity:
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Pred. No.:
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US-10-156-761-1
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## Publication No. US20040123343A1

| GENERAL INFORMATION:
| APPLICANT: La Rosa, Thomas J. |
| APPLICANT: Cavalic, David K. |
| APPLICANT: Zhou, Yihua |
| APPLICANT: Zhou, Yihua |
| APPLICANT: Boukharov, Andrey A. |
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APPLICANT: Conner, Timothy W.
APPLICANT: Conner, Timothy W.
APPLICANT: Heck, Gregory R.
TILE APPLICANT: Liu, Jingdong
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Transcription in Plants
TITLE OF INVENTION: Transcription in Plants
TITLE OF INVENTION: Transcription in Plants
TITLE OF INVENTION: Transcription in Plants
TITLE OF INVENTION: Transcription in Plants
TITLE OF INVENTION: WHERE: US 60/067,000
PRIOR APPLICATION NUMBER: US 60/067,000
PRIOR APPLICATION NUMBER: US 60/074,201
PRIOR APPLICATION NUMBER: US 60/074,201
PRIOR APPLICATION NUMBER: US 60/074,201
PRIOR FILING DATE: 1998-02-10
PRIOR FILING DATE: 1998-02-10
PRIOR FILING DATE: 1998-02-10
PRIOR FILING DATE: 1998-02-10
PRIOR FILING DATE: 1998-02-10
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Matches:
Conservative:
Mismatches:
Indels:
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_35608C.1
US-10-437-963-31286
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Publication No. US20040123339A1
GENERAL INFORMATION:
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ORGANISM: Oryza sativa
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ATE: 1998-06-30 ION NUMBER: US 60/091,247

A PELLING DATE: 1998-02-19

RAPLICATION NUMBER: US 60/075,459

RILING DATE: 1998-02-19

R FILING DATE: 1998-02-19

R PILING DATE: 1998-02-19

R APPLICATION NUMBER: US 60/075,464

R APPLICATION NUMBER: US 60/075,464

R APPLICATION NUMBER: US 60/075,460

R RILING DATE: 1998-02-19

R RELING DATE: 1998-02-19

R FILING DATE: 1998-02-19 FILING DATE: 1998-06-18
APPLICATION NUMBER: US 60/089,812
FILING DATE: 1998-06-18
APPLICATION NUMBER: US 60/089,807
FILING DATE: 1998-06-18
APPLICATION NUMBER: US 60/089,806 NA PELICATION NUMBER: US 60/077,229

R FILING DATE: 1998-03-09

R APPLICATION NUMBER: US 60/077,230

R APPLICATION NUMBER: US 60/079,368

R APPLICATION NUMBER: US 60/078,368

R FILING DATE: 1998-03-18

R FILING DATE: 1998-04-07

R APPLICATION NUMBER: US 60/080,844

PRILING DATE: 1998-04-07

R APPLICATION NUMBER: US 60/083,067 LLNG DATE: 1998-05-15 PPLICATION NUMBER: US 60/086,186 LLNG DATE: 1998-05-21 LING DATE: 1998-05-21
LICATION NUMBER: US 60/086,187
LING DATE: 1998-05-31 APPLICATION NUMBER: US 60/086,183 FILING DATE: 1998-05-21 FILING DATE: 1998-05-21 PAPLICATION NUMBER: US 60/086,188 FILING DATE: 1998-05-21 APPLICATION NUMBER: US 60/086,524 LING DATE: 1998-06-16
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LING DATE: 1998-06-18
PPLICATION NUMBER: US 60/089,814 PILING DATE: 1998-06-18
APPLICATION NUMBER: US 60/089,811
FILING DATE: 1998-06-18
PILING DATE: 1998-06-18
APPLICATION NUMBER: US 60/089,793
APPLICATION NUMBER: US 60/091,405 APPLICATION NUMBER: US 60/083,388 FILING DATE: 1998-04-29 APPLICATION NUMBER: US 60/083,389 LICATION NUMBER: US 60/086,185
LING DATE: 1998-05-21
LING DATE: 1998-05-21
LING DATE: 1998-05-21 FILING DATE: 1998-06-18 APPLICATION NUMBER: US 60/089,808 LING DATE: 1998-06-18
PLICATION NUMBER: US 60/089,813
LING DATE: 1998-06-18 FILING DATE: 1998-04-27
PELLING DATE: 1998-04-27
FILING DATE: 1998-04-29
APPLICATION NUMBER: US 60/083,387 FILING DATE: 1998-04-29 APPLICATION NUMBER: US 60/085,224 FILING DATE: 1998-05-13 LICATION NUMBER: US 60/085, 222 APPLICATION NUMBER: US 60/074,789 FILING DATE: 1998-02-19 APPLICATION NUMBER: US 60/077,231 FILING DATE: 1998-03-09 APPLICATION NUMBER: US 60/085,223 FILING DATE: 1998-05-13 CATION NUMBER: US 60/085,533 FILING DATE: 1998-04-29 1998-05-13 ING DATE: PRILICA PRILIC

Length:
Matches:
Conservative:
Mismatches:
Indels: US-09-972-032-2 (1-79) x US-09-922-293-1599 (1-254) PRICE APPLICATION NUMBER: US 60/091,647
PRICE PLING DATE: 1998-09-09
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PRICE PLING DATE: 1998-10-13
PRICE Gaps: 25.5 8.00 100.00% 100.00% 10.13% Percent Similarity:
Best Local Similarity:
Query Match:
DB: TYPE: DNA ORGANISM: Zea mays US-09-922-293-1599 Alignment Scores: Pred. No.: PRIOR PRIOR PRIOR

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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ORGANISM: Zea mays
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TITLE OF INVENTION: 1 dentification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.0348
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-18
PRIOR FILING DATE: 0000-03-18
PRIOR PLICATION NUMBER: 60/206,848
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Gaps:
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, UUN
APPLICANT: ISHIKAWA, UUN
APPLICANT: SHIRAWA, HIROSHI
APPLICANT: SHEA, TADAYOSHI
APPLICANT: SHEA, TADAYOSHI
APPLICANT: SHEA, TADAYOSHI
APPLICANT: HATTORI, WOSHITWI
APPLICANT: HATTORI, WOSHITWI
APPLICANT: HATTORI, WOSHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-26
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-06-30
NUMBER: OF 2001-07-20
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US-10-282-122A-11225/c
Sequence 11225, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
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52 ArgSerAlaSerArgTrpProTrp 59
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                                                                                                                                                                                 ; Sequence 6581, Application US/10156761; Publication No. US20030119018A1; GENERAL INFORMATION:
                                                  31 CGATCAGCGAGCCGTTGGCCATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Streptomyces avermitilis
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Query Match:
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Sequence 38330, Application US/10437963
; Sequence 38330, Application US/10437963
; Publication No. US2004012334341
; Publication No. US2004012334341
; Publication No. US2004012334341
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5321)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 38330
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Squence 21611, Application US/10425114

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Avoalic, David K.

APPLICANT: Tabaska, Jack E
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Mismatches:
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OTHER INFORMATION: Clone ID: LIB3354-046-G9_FLI
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Matches:
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ORGANISM: Oryza sativa
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Best Local Similarity:
Query Match:
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ORGANISM: Zea mays
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US-10-425-114-21611
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Ouery Match:
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Sequence 3767, Application No. US20030233675A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Greyory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Marry S.
APPLICANT: Goldman, Marry S.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: BLANTS US/10/369,493
CURRENT APPLICATION NUMBER: US/10/369,039
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 37767
                                                                                                                                                                                                                                        Sequence 35593, Application US/10369493

Sequence 35593, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATON:
APPLICANT: Cao, Yongwei
APPLICANT: Alater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
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APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2002-02-21
FRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 35593
LENTH: 777
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      US-09-972-032-2 (1-79) x US-10-425-114-13766 (1-775)
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Gaps:
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                                                                                                                                312 cácricácicacidarcacididade 289
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                                                                      49 ArgTrpProArgSerAlaSerArg 56
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Best Local Similarity:
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Pred. No.:
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RESULT 13
US-09-773-926-8/C
US-09-773-926-8/C
Sequence 8, Application US/09773926
Facent No. US2002004207A1
Facent No. US2002004207A1
FALSE LINCOMMATION: MALP-GENE, NUCLEIC ACIDS, POLYPEPTIDES AND USE THEREOF
TITLE OF INVENTION: MALP-GENE, NUCLEIC ACIDS, POLYPEPTIDES AND USE THEREOF
CURRENT APPLICATION NUMBER: US/09/773,926
CURRENT FILING DATE: 2001-02-02
FRIOR PILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 17
SOOTHWARE: PATENTING DATE: 2.000-02-11
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Publication No. US20030101476A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Short, Jay
APPLICANT: Richardson, Toby
APPLICANT: Richardson, Toby
APPLICANT: Richardson, Toby
TITLE OF INVENTION: Recombinant Phytases and Uses Thereof
TITLE OF INVENTION: Necombinant Phytases and Uses Thereof
TITLE OF INVENTION: NECOMBINANT SOURCE 1020
CURRENT APPLICATION NUMBER: US/10/021,723A
CURRENT PPLICATION NUMBER: US 60/255,090
PRIOR PPLICANION NUMBER: US 60/255,090
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 74
SOFTWARE: REAUSED for Windows Version 4.0
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US-09-972-032-2 (1-79) x US-10-282-122A-13444 (1-1035)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            910 CTGGGGGAAGGCAGGAGGAGGC 887
                                            48 SerArgTrpProArgSerAlaSer 55
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ORGANISM: Homo sapiens
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; ORGANISM: Rhizobium
US-10-021-723A-7
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Best Local Similarity:
Query Match:
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Search completed: July 12, 2004, 21:27:05 Job time : 2948 secs

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us-09-972-032-2.rni

Sequence 3, Appli Sequence 53, Appl Sequence 5899, Ap Sequence 5899, Ap Sequence 5117, A Sequence 12112, A Sequence 12112, A Sequence 12112, A Sequence 12112, A Sequence 12112, A Sequence 12112, A Sequence 1488, Ap Sequence 1488, Ap Sequence 2991, Ap Sequence 2991, Ap Sequence 2991, Ap Sequence 2991, Ap Sequence 2614, Ap Sequence 2614, Ap Sequence 265, App Sequence 265, App Sequence 1688, App Sequence 1688, App Sequence 1688, App Sequence 1688, App Sequence 523, App Sequence 523, App Sequence 523, App Sequence 5488, Ap Sequence 5488, Ap Sequence 5488, Ap Sequence 5488, Ap Sequence 5488, Ap 05.244792.9
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05.09.313.294A.498
05.09.313.294A.5899
05.09.313.294A.5899
05.09.313.294A.5899
05.09.313.294A.5899
05.09.313.294A.5899
05.09.621.976.14323
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05.09.621.976.14323
05.09.252.991A.14813
05.09.252.991A.6345
05.09.252.991A.6345
05.09.252.991A.64653
05.09.252.991A.64653
05.09.252.991A.16094
05.09.252.991A.16094
05.09.252.991A.16094
05.09.252.991A.16094
05.09.252.991A.16094
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05.09.252.991A.16094
05.09.252.991A.16094
05.09.252.991A.16094
05.09.252.991A.16094
05.09.252.991A.16094
05.09.252.991A.16094

ALIGNMENTS

RESULT 1
US-08-47-965A-1/C

| US-08-47-965A-1/C
| Sequence 1, Application US/08447965A
| Patent No. 5776692
| GENERAL INFORMATION:
| APPLICANT: Graham, David Y.
| APPLICANT: Graham, David Y.
| APPLICANT: Graham, David Y.
| APPLICANT: Graham, David Y.
| APPLICANT: Graham, David Y.
| APPLICANT: Graham, David Y.
| APPLICANT: Graham, David Y.
| APPLICANT: Graham, David Y.
| APPLICANT: Graham, David Y.
| TITLE OF INVENTION: and its Expressed Product
| TITLE OF INVENTION: and its Expressed Product
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| TITLE OF INVENTION: AND INVENTION: AND INVENTION: AND INVENTION: AND INVENTION: AND INVENTION: AND INVENTION: AND INVENTION: BLACK OF INVENTION: BLACK OF INVENTION: APPLICATION NUMBER: 36,119
| REFERENCE/DOCKET NUMBER: 36,119
| REFERENCE/DOCKET NUMBER: 36,119
| REFERENCE/DOCKET NUMBER: 36,119
| REFERENCE/DOCKET NUMBER: 311.019
| TELEPHONE: 202-662-4643
| INPORMATION FOR ENG ID NO: 1:
| SEQUENCE CHARACTERISTICS:
| LENGTH: 1402 base pairs

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Tue Jul 13 16:16:22 2004

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Alignment Scores:
Pred. No.:
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Pred. No.:
Score:
         US-08-107-676-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Content, Jean
APPLICANT: DeFit, Locas
APPLICANT: DeFit, Locas
APPLICANT: DeFit, Jacqueline
TITLE OF INVENTION: Mycobacterium Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding Them for Diagnosis and Control of
TITLE OF INVENTION: Tuberculosis
TITLE OF INVENTION: Suberculosis
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BEN FC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,676
FILING DATE: US/08/107,676
FILING DATE: US-OFT-1993
CLASSIFICATION NUMBER: WO PCT/EP92/00268
FILING DATE: OF-PEB-199
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BP 91400388.4
FILING DATE: US-PEB-199
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: BS 91400388.4
FILING DATE: US-PEB-199
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: BS 91400388.4
FILING DATE: US-PEB-199
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: BS 91400388.4
FERENCCOMMUNICATION INFORMATION:
TELEPHONE: G10-332-5300
                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5955356west Center
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Mycobacterium kansasii
IMMEDIATE SOURCE:
CLONE: Antigen 85B from M. kansasii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-107-676-25

Sequence 25, Application US/08107676

Patent No. 5955356

GENERAL INFORMATION:

APPLICANT: Content, Jean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 25.
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                   DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
E: DNA (genomic)
                                                                                                                                                                      10.2
9.00
100.00%
100.00%
11.39%
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genor
HYPOTHETICAL: NO
                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
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MOLECULE TYPE: D
ORIGINAL SOURCE:
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                                                                                                                                                      Alignment Scores:
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RESULT 3
19.09-295-820-25
; Sequence 25, Application US/09295820
; Patent No. 6638511
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; Dewit, Lucas
; DeBruyn, Jacqueline
; TITLE OF INVENTION: Mycobacterium Polypeptides and Nucleic
; TITLE OF INVENTION: Mycobacterium Polypeptides and Control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPER: PLOPPY disk

MEDIUM TYPER: PLOPPY disk

COMPUTER: ISM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/25,820

FILING DATE: 21-Apr-1999

PRIOR APPLICATION NUMBER: 08/107,676

PILING DATE: Unknown>

APPLICATION NUMBER: BP 91400388.4

FILING DATE: 14-FEB-1991

ATTORNEY/AGENT INFORMATION:

NAME: KOWALCHY, KACHERINE M.

REGISTRATION NUMBER: 36,848

REFERENCE/DOCKET NUMBER: 36,848

REFERENCE/DOCKET NUMBER: 36,848

REFERENCE/DOCKET NUMBER: 36,848

REFERENCE/DOCKET NUMBER: 3076.89USWO

TELEPHONE: 612-332-5300

TELEPAS: 612-332-5300

INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERSTICE:
                     Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                         US-09-972-032-2 (1-79) x US-08-107-676-25 (1-1335)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSE: Merchant & Gould
STREET: 3100 No. 6638511west Center
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLONE: Antigen 85B from M. kansasii
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-295-820-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Length:
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                 751 CCGCGGTCGCCATCTCGATGGCCG 774
                                                                                                                                                                                                  51 ProArgSerAlaSerArgTrpPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                        100.00%
100.00%
10.13%
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                                 Percent Similarity:
Best Local Similarity:
Query Match:
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RESULT 6
US-09-252-991A-5051
Sequence 5051, Application US/09252991A
Sequence 5051, Application US/09252991A
Sequence 5051, Application US/09252991A
Sequence 5051, Application US/09252991A
Setemation: Marc J. Rubenfield et al.
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: WUMBER: US/09/252,991A
CURRENT PELING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER: OF SEQ ID NOS: 33142
SEQ ID NO 5031
LENGTH: 1617
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Sequence 19, Application US/09291922

Patent No. 6383776

GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Hitz, Bill
APPLICANT: Hitz, Bill
APPLICANT: Tingey, Scott
TITLE OF INVENTION: Plant Sugar Transport Proteins
FILE REFERENCE: Bell63
CURRENT APPLICATION NUMBER: US/09/291,922
CURRENT FILING DATE: 1999-04-14
BEALIER FILING DATE: 1999-04-14
BARLIER PILING DATE: April 24, 1998
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Microsoft Office 97
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
                                                            US-09-972-032-2 (1-79) x US-09-252-991A-5081 (1-1608)
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                                                                                                                                                         668 rcaadardaccadarcadcarca 691
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Best Local Similarity:
Query Match:
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US-09-291-922-19
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Pred. No.:
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Sequence 5665, Application US/09489039A
Sequence 5665, Application US/09489039A
Patent No. 6108186
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
FRICR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 5665
LINGTH: 1539
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Matches:
Conservative:
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Indels:
          Conservative:
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Indels:
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Matches:
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Mismatches:
Indels:
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                                                                                                                                    US-09-972-032-2 (1-79) x US-09-295-820-25 (1-1335)
                                                                                       Gaps:
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                                                                                                                                                                                                                751 CCGCGGTCGGCATCTCGATGGCCG 774
                                                                                                                                                                                   51 ProArgSerAlaSerArgTrpPro 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Klebsiella pneumoniae
       100.00%
100.00%
10.13%
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8.00
100.00%
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8.00
100.00%
100.00%
10.13%
Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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US-09-252-991A-5081
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Pred. No.:
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Sequence 1522, Application US/09252991A

Parent No. 6551795

GENERAL INFORMATION:
APPLICANT:
MARC J. Rubenfield et al.
APPLICANT:
MARC J. Rubenfield et al.
TITLE OF INVENTION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION:
APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PELING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 15522
LENGTH: 2784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDC 1551 $\tt "n"$ bases at various positions throughout the sequence represent a, t, c or g
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                 US-09-972-032-2 (1-79) x US-09-252-991A-15430 (1-2463)
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Mismatches:
Indels:
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Matches:
Conservative:
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                                                                                        1073 gerregagaregecerregagesek 1050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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Query Match:
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OTHER INFORMATION:
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Pred. No.:
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Pred. No.:
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                                                                                                                                                          Sequence 15346, Application US/09252991A

Sequence 15346, Application US/09252991A

Sequence 15346, Application US/09252991A

Sequence 15346, Application US/09252991A

Patent No. 6551795

GENERAL INPORMATION:

MACC J. Rubenfield et al.

TITLE OF INVENTION:

NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION:

TITLE OF INVENTION:

RILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-02-18

NUMBER OF SEQ ID NOS: 33142

LENGTH: 2283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15430, Application US/09252991A
Sequence 15430, Application US/09252991A
Sequence 15430, Application US/09252991A
Setent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J.
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILLE REFRENCE: 107196.13
FILLE REFRENCE: 107196.13
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
SEQ ID NO 15430
SEQ ID NO 15430
SEQ ID NO 15430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-972-032-2 (1-79) x US-09-252-991A-15346 (1-2283)
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Matches:
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Mismatches:
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Matches:
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Mismatches:
Indels:
Gaps:
                                   US-09-972-032-2 (1-79) x US-09-291-922-19 (1-1914)
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Gaps:
                                                                                                          1393 GGCCTTGGAGAGGACAGGAAGGT 1370
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                                                                         25 GlyLeuGlyGluGlyGluGly 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Pseudomonas aeruginosa US-09-252-991A-15430
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US-09-252-991A-15430/c
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DB:
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; LOCATION: (1)..(262)
; OTHER INFORMATION: n = a,
US-09-280-116-53
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ORGANISM: Homo sapiens
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Best Local Similarity:
                                 Percent Similarity:
Best Local Similarity:
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5244792-9
; Patent No. 5244792
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; LENGTH: 223
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Pred. No.:
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LENGTH: 262
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DB:
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Sequence 1, Application US/09103840A

Partial INFORMATION:
APPLICANT: FLEISCHWAN, Robert D.
APPLICANT: FLEISCHWAN, Robert D.
APPLICANT: FRASER, Claire M.
APPLICANT: PRASER, Claire M.
APPLICANT: PRASER, John C.
TITLE OF INVENTION: DAS ESQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: DAS ESQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBRERCUSIS
FILE REPERBENCE: 24366-20007.00
CURRENT FILING DATE: 1988-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1

LENGTH: 4411529
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, OTHER INFORMATION: Description of Artificial Sequence:primer US-09-344-888A-3
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                                                                        US-09-972-032-2 (1-79) x US-09-103-840A-2 (1-4403765)
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Matches:
Conservative:
Mismatches:
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Patent No. 6291245
GENERAL INFORMATION:
APPLICANT: KOPETAIL, Erhard
APPLICANT: Schantz, Christian
TITLE OF INVENTION: Now Host-Vector System
FILE REFERENCE: CL20315
CURRENT APPLICATION NUMBER: US/09/344,888A
CURRENT FILING DATE: 1999-06-25
FRIOR APPLICATION NUMBER: EP98113156.8
FRIOR FILING DATE: 1998-07-15
FRIOR APPLICATION NUMBER: EP98119078.8
FRIOR FILING DATE: 1998-07-15
FRIOR APPLICATION NUMBER: EP98119078.8
FRIOR SELING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 24
                                                                                                                                         943238 CCGCGTTCCGCATCGCCTGGCCG 94321S
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                                                                                                            51 ProArgSerAlaSerArgTrpPro 58
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ORGANISM: Mycobacterium tuberculosis
OTHEN INFORMATION: H37Rv
US-09-103-840A-1
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Best Local Similarity: 100.00%
Query Match: 10.13%
DB: 3
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Pred. No.:
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US-09-344-888A-3
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LENGTH: 53
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RESULT 15
US-09-280-116-53/c
US-09-280-116-53/c
Sequence 53, Application US/09280116A
Sequence 53, Application US/09280116A
GENERAL INFORMATION:
APPLICANT: Robison.
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
FILE REFERENCE: 5800-24 035800/176965
CURRENT FALICATION NUMBER: US/09/280,116A
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 268
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TITLE OF INVENTION: EXPRESSION OF RECOMBINANT GLYOPROTEIN
B FROM HAFRES SIMPLEX VIRUS
NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/587,179
FILING DATE: 20-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 921,730
FILING DATE: 20-OCT-1986
APPLICATION NUMBER: 597,784
FILING DATE: 06-AFR-1984
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OTHER INFORMATION: aspartyl proteases
FEATURE:
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Pred. No.:
Score:
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Conservative:	Mismatches:	Indels:	
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DB: 4 Gaps: US-09-972-032-2 (1-79) x US-09-280-116-53 (1-262)

Search completed: July 12, 2004, 18:46:21 Job time: 1734 secs

Human cDN Human tra Human imm

Aad58740 | Aak87029 |

Pelymorph
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Aaas6368 Aas27829 Aas27829 Adb94632 Adb94630 Adb94630 Aal36258 Aal36258 Aal97583 Aaa96333 Aaa96333 Aaa9633 Aaas63030 Add71050 Aak84551 Aas32644 Aas32644 Aas32644 Aas32644

Human gen Novel hum Human pol Human pro Human pol

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New polypeptide, that is a functional equivalent of ERCOA3 (Estrogen Receptor Coregulator 3), is useful in inhibiting or reducing tamoxifen or estrogen-induced proliferation of cancer cells and in treating
                                                                                                                                                                                                                                                                                                                                                                                 Estrogen Receptor Coregulator 3; ERCoA3; tamoxifen; estrogen; cancer; osteoporosis; cytostatic; osteopathic; human; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                              203. .442 /
/*tag= a
/product= "ERCOA3 protein"
                                                                                                                                                                                                                                                ALIGNMENTS
                            AAA96368
AAS27829
AAB94632
ADB94630
ADB94630
AAD1699
AAL3628
AAL3628
AAA9638
AAA9638
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                                                                                                                                                                                                                                                                                                   ABL60606 standard; cDNA; 990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-OCT-2000; 2000US-0238190P.
                                                                                                                                                                                                                                                                                                                                         (first entry)
Montano M, Sutton A;
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P-PSDB; ABB08035.

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ABL60606;
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Aas69040 DNA encod
Aal01097 Human rep
Abl6553 Human tes
Abl61947 Colon ade
Abl61947 Colon ade
Abl61948 Colon ade
Aba15806 Human GPC
Adc87010 Human GPC
Adc87010 Human ner
Aba15806 Human ner
Aba15806 Human ner
Aba15806 Human ner
Aba2699 Human ner
Adc86996 Human RPC
Adc27000 Human Car
Adc86999 Human PRD
Adb72818 Human PRD
Adb72818 Human PRD
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Compugen Ltd.
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                                                                                                                                                                                  3373863 seqs, 2124099041 residues
        GenCore version
Copyright (c) 1993 - 2004
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                                                nucleic search, using sw model
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AAS69040
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Gapop_60.0 , Gapext 60.0
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1: geneseqn1980s:*

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The invention relates to a ERCOA3 (Estrogen Receptor Coregulator 3) protein and encoding polymuclectides. ERCOA3 can be used to inhibit reduce tamoxifen or estrogen induced proliferation of cancer cells, reduced activity of ERCOA3, and for detecting cancer cells that are

Claim 5; Fig 1; 39pp; English.

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Query Match
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                                                                                                                                          AAS69040;
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tamoxifen resistant, or to treat osteoporosis, by increasing levels of BRCoA3 in cells. The encoding polynucleotide can be used to inhibit translation of a mRNA encoding ERCoA3. BECOA3 acts as a coregulator protein and can bind to the estrogen receptor to activate a molecular or cellular response in the cell. The present sequence represents the human
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                                                                                                DB 6; Length 990;
                                                                           Sequence 990 BP; 189 A; 281 C; 317 G; 203 T; 0 U; 0 Other;
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CCTCAGCHTC
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also useful of agnostics as expressed sequence tags for identifying expressed gene therapy techniques to restore normal activity of (II) or to tract disease states involving (II). (II) is useful in gene therapy techniques to restore normal activity of (II) or to tract disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders in polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
960
                                                                          coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mapping; gene mapping; gene therapy; forensic;
medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding novel human diagnostic protein #4844.
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Pred. No. 4e-48;
                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                            961 AAAAAAAAAAAAATGAGCGGCCGCAAGTT
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23-AUG-2000; 2000US-00649167.
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P-PSDB; ABG04853.
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01-SEP-2000; 2000US-0229344P.
01-SEP-2000; 2000US-0229344P.
05-SEP-2000; 2000US-022954PP.
06-SEP-2000; 2000US-0229509P.
06-SEP-2000; 2000US-0229509P.
06-SEP-2000; 2000US-0229509P.
06-SEP-2000; 2000US-0229509P.
06-SEP-2000; 2000US-0231244P.
08-SEP-2000; 2000US-02313064P.
08-SEP-2000; 2000US-02313064P.
08-SEP-2000; 2000US-02313064P.
08-SEP-2000; 2000US-02313064P.
08-SEP-2000; 2000US-02313064P.
08-NOV-2000; 2000US-0246474P.
08-NOV-2000; 2000US-0246524P.
08-NOV-2000; 2000US-0246524P.
08-NOV-2000; 2000US-0246528P.
08-NOV-2000; 2000US-0246528P.
08-NOV-2000; 2000US-0246528P.
08-NOV-2000; 2000US-0246528P.
08-NOV-2000; 2000US-0246528P.
08-NOV-2000; 2000US-0246528P.
08-NOV-
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      Indels
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2000US-0180628P

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2000US-0199123P

2000US-0199123P

2000US-0199135P

2000US-0205515P

2000US-0205515P

2000US-02174867P

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  Matches 147; Conservative
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gastrointestinal disease; infection; cytostatic; gene; ss
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2000US-0205515P.
2000US-0209467P.
2000US-0214886F.
2000US-0215135P.
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2000US-02312448
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2000US-0180628P.
2000US-0184664P.
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2000US-0189874P.
2000US-0190076P.
                                                                                                                                                                        17-JAN-2001; 2001WO-US001329
                                                                                      WO200155317-A2
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14-SEP-2000; 2
14-SEP-2000; 2
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12-SEP-2000; 2
14-SEP-2000; 2
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                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a coding sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, testicular antigen; testes; cancer; metastasis; immune disorder; reproductive system disorder; urinary system disorder; gene therapy; cardiovascular disorder; respiratory disorder; neurological disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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8.3e-22;
hes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 404 BP; 83 A; 109 C; 107 G; 95 T; 0 U; 10 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human testicular antigen encoding cDNA SEQ ID NO: 231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.1%; Score 80; DB Best Local Similarity 100.0%; Pred. No. 8.3 Matches 80; Conservative 0; Mismatches
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17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249216P.
17-NOV-2000; 2000US-0249216P.
17-NOV-2000; 2000US-0249216P.
17-NOV-2000; 2000US-0249216P.
17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-0249269P.
17-NOV-2000; 2000US-024920P.
17-NOV-2000; 2000US-024920P.
17-NOV-2000; 2000US-024920P.
17-NOV-2000; 2000US-025198P.
05-DEC-2000; 2000US-025198P.
05-DEC-2000; 2000US-025198P.
06-DEC-2000; 2000US-025198P.
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P-PSDB; AAM95127.
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PR 25-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235484P.
PR 29-SEP-2000; 2000US-0235484P.
PR 29-SEP-2000; 2000US-0235436P.
PR 29-SEP-2000; 2000US-0235468P.
PR 29-SEP-2000; 2000US-0235468P.
PR 29-SEP-2000; 2000US-0235468P.
PR 29-SEP-2000; 2000US-0235468P.
PR 29-SEP-2000; 2000US-0235468P.
PR 29-CCT-2000; 2000US-0235468P.
PR 20-CCT-2000; 2000US-0234708P.
PR 20-CCT-2000; 2000US-024478P.
PR 20-CCT-2000; 2000US-024477P.
PR 20-CCT-2000; 2000US-024477P.
PR 20-CCT-2000; 2000US-024477P.
PR 20-CCT-2000; 2000US-024477P.
PR 20-CCT-2000; 2000US-024477P.
PR 20-CCT-2000; 2000US-024477P.
PR 20-CCT-2000; 2000US-024477P.
PR 20-CCT-2000; 2000US-024427P.
PR 20-NOV-2000; 2000US-024221P.
PR 20-NOV-2000; 2000US-024221P.
PR 20-NOV-2000; 2000US-024221P.
PR 20-NOV-2000; 2000US-024221P.
PR 20-NOV-2000; 2000US-024224P.
PR 20-NOV-2000; 2000US-024224P.
PR 20-NOV-2000; 2000US-024224P.
PR 20-NOV-2000; 2000US-024224P.
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PR 20-NOV-2000; 2000US-024224P.
PR 20-NOV-2000; 2000US-024224P.
PR 20-NOV-2000; 2000US-024224P.
PR 20-NOV-2000; 2000US-024224P.
PR 20-NOV-2000; 2000US-024224P.
PR 20-NOV-2000; 2000US-024224P.
PR 20-NOV-2000; 2000US-024224P.
PR 20-NOV-2000; 2000US-024224P.
PR 20-NOV-2000; 2000US-024224P.
PR 20-NOV-2000; 2000US-024224P.
PR 20-NOV-200
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931
                                                                                                                                                                         The present invention provides the protein and coding sequences of 973 human testicular antigens, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a cDNA of the
                                                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma; gene; ds.
                                                                                                  Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer.
                                                                                                                                                                                                                                                                                                                                                                                                           872 CAAAGTCCTGTCCCGTTGGCTGCCTTCATCCACTCTCTCACTTCTCTGCCTTCAGAGTAA
                                                                                                                                                                                                                                                                                                                                                             .
0
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                                                                                                                                                                                                                                                                                                Sequence 404 BP; 83 A; 109 C; 107 G; 95 T; 0 U; 10 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Colon adenocarcinoma related gene sequence SEQ ID NO:284.
                                                                                                                                                 Claim 1; SEQ ID NO 231; 766pp; English
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                                           Ruben SM
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18-SEP-2000; 2000US-023313P.
18-SEP-2000; 2000US-023313P.
20-SEP-2000; 2000US-023403P.
20-SEP-2000; 2000US-023403P.
22-SEP-2000; 2000US-023403P.
22-SEP-2000; 2000US-023403P.
22-SEP-2000; 2000US-023492P.
25-SEP-2000; 2000US-0234924P.
25-SEP-2000; 2000US-0234924P.
25-SEP-2000; 2000US-0234924P.
25-SEP-2000; 2000US-0235082P.
25-SEP-2000; 2000US-0235082P.
25-SEP-2000; 2000US-0235134P.
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              (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                                                             80; Conservative
                                           Rosen CA, Barash SC,
                                                                      WPI; 2001-483232/52.
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Best Local Similarity
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                                                                                                                                                                                                                                                                       invention
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                                                                                                                                                                                                                                                                                                                                                             Matches
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Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;

WO200194629-A2 Homo sapiens.

gene; ds

13-DEC-2001

Kidney cancer related gene sequence SEQ ID NO:6702,

(first entry)

15-MAY-2002

ABL68365;

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The present invention describes a method (M1) for screening for an antinoplastic agent. The method involves exposing cells to a chemical agent to be tested for antineoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative antineoplastic activity. (I) has cytostatic activity and can be used in antineoplastic agent, and can be used for producing a product which is antineoplastic agent, and can be used for producing a product which is antineoplastic agent. In can be used for producing a product which is confirmed to the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating lobular cancer, squamous cell cancer, infiltrating lobular cancer, squamous coll cancer, infiltrating lobular cancer, squamous cancer, accinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 284; 44pp; English
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                                                        27-SEP-2000, 2000US-0235720P.
27-SEP-2000, 2000US-0235840P.
27-SEP-2000, 2000US-0235840P.
28-SEP-2000, 2000US-0236028P.
28-SEP-2000, 2000US-023603P.
28-SEP-2000, 2000US-023603P.
28-SEP-2000, 2000US-0236109P.
28-SEP-2000, 2000US-0236109P.
29-SEP-2000, 2000US-0236109P.
29-SEP-2000, 2000US-023619P.
02-OCT-2000, 2000US-0237173P.
02-OCT-2000, 2000US-0237173P.
02-OCT-2000, 2000US-0237173P.
02-OCT-2000, 2000US-0237173P.
02-OCT-2000, 2000US-0237173P.
02-OCT-2000, 2000US-0237173P.
02-OCT-2000, 2000US-0237173P.
02-OCT-2000, 2000US-0237173P.
03-OCT-2000, 2000US-023718P.
03-OCT-2000, 2000US-023718P.
03-OCT-2000, 2000US-023718P.
03-OCT-2000, 2000US-023718P.
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03-OCT-2000; 2000US-0237606P.
03-OCT-2000; 2000US-0237608P.
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Soppet DR, Weaver Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AVAL-) AVALON PHARM.
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Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ebner R,
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                                                                                                                                                                                                                                                                                                       25-SEP-2000; 20000S-0234923P.
25-SEP-2000; 20000S-0234923P.
25-SEP-2000; 20000S-0234924P.
25-SEP-2000; 20000S-0235082P.
25-SEP-2000; 20000S-0235084P.
26-SEP-2000; 20000S-023508P.
27-SEP-2000; 20000S-023563P.
27-SEP-2000; 20000S-023563P.
27-SEP-2000; 20000S-023563P.
27-SEP-2000; 20000S-023563P.
27-SEP-2000; 20000S-023563P.
28-SEP-2000; 20000S-023563P.
28-SEP-2000; 20000S-023603P.
29-SEP-2000; 20000S-023603P.
29-SEP-2000; 20000S-023603P.
20-CCT-2000; 20000S-023729P.
02-CCT-2000; 20000S-023729SP.
03-CCT-2000; 20000S-023729SP.
03-CCT-2000; 20000S-023729SP.
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2000US-0234052P.
2000US-0234509P.
2000US-0234567P.
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03-OCT-2000; 2000US-0237606P
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Weaver Z;
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22-SEP-2000;
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25-SEP-2000;
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Soppet DR,
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ABL68365 standard; DNA; 149480 BP. RESULT 6 ABL68365 ID ABL6

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Gaps

o;

5.2%; Score 51; DB 6; Length 149480; 100.0%; Pred. No. 7.6e-11; cive 0; Mismatches 0; Indels 0.

51; Conservative

Matches

8

Query Match Best Local Similarity

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RESULT 8
ADC87623/c
ID ADC87623 standard; DNA; 118584
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                              The present invention describes a method (M1) for screening for an antinoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL7010), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an activity and can be used in gene therapy. M1 can be used for screening and activity and the data is sufficient to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, clear cell cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                                                                                         Sequence 149480 BP; 39770 A; 34233 C; 35027 G; 40449 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                             0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                       76386 CCCGCCTCAGCTTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCGCGCC 76436
                                                                                                                                                                                                                                                                                                                                                      57 CCCGCCTCAGCTTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCGCGCC 107
                                                                                                                                                                                                                                                                                                 Ouery Match 5.2%; Score 51; DB 6; Length 149480; Best Local Similarity 100.0%; Pred. No. 7.6e-11; Matches 51; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Colon adenocarcinoma related gene sequence SEQ ID NO:285.
           Claim 1; SEQ ID NO 6702; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL61948 standard; DNA; 149480 BP
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2000US-0233113P.
2000US-0234009P.
2000US-023403P.
2000US-0234009P.
2000US-023403P.
2000US-0234502P.
2000US-0234503P.
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2000US-0235134P.
2000US-0235280P.
2000US-0235637P.
2000US-0235638P.
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18-SEP-2000; 2
20-SEP-2000; 2
20-SEP-2000; 2
20-SEP-2000; 2
22-SEP-2000; 2
25-SEP-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-SEP-2000; 26-SEP-2000; 27-SEP-2000; 27-SEP-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL61948;
                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
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The present invention describes a method (M1) for screening for an antinoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 of ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the act collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, and cancer, and cancer, infiltrating lobular cancer, squamous call carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Horrigan S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carter KC, Ebner R, Endress G,
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5.2%; Score 51; DB 6; Length 149
Best Local Similarity 100.0%; Pred. No. 7.6e-11;
Matches 51; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 285; 44pp; English.
27-5EP-2000, 2000US-0235840P.
28-5EP-2000, 2000US-0235863P.
28-5EP-2000, 2000US-0236032P.
28-5EP-2000, 2000US-0236034P.
28-5EP-2000, 2000US-0236034P.
28-5EP-2000, 2000US-0236034P.
28-5EP-2000, 2000US-023611P.
29-5EP-2000, 2000US-023611P.
29-5EP-2000, 2000US-023611P.
29-5EP-2000, 2000US-023684P.
02-0CT-2000, 2000US-0237294P.
02-0CT-2000, 2000US-0237294P.
02-0CT-2000, 2000US-023729F.
03-0CT-2000, 2000US-0237366P.
03-0CT-2000, 2000US-0237425P.
03-0CT-2000, 2000US-0237425P.
03-0CT-2000, 2000US-0237466P.
03-0CT-2000, 2000US-0237664P.
03-0CT-2000, 2000US-0237668P.
03-0CT-2000, 2000US-0237668P.
01-NOV-2000, 2000US-0237668P.
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Weaver 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-188264/24.
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ADC87623

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Claim 1; SEQ ID NO 1463; 28pp;
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2000US-0215135P.
2000US-0216647P.
2000US-0216880P.
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2000US-0209467P.
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2000US-0184664P
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2000US-0189874P
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                                                                                                                           2003-315783/31.
                                                                                                                                                                                          New polynucleotide,
patient in need of i
                                                                            Asai K,
                                                                                                                                                      P-PSDB; ADC87011
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07-JUL-2000;
07-JUL-2000;
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17-MAR-2000;
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07-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABA15806;
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  (NAAD-)
(ADSC-)
                                                                            Suwa M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel polymucleotide encoding a guanosine triphosphate-binding protein coupled receptor (GPCR). A polymucleotide of the invention may have a use in gene therapy. The polymucleotide and polymeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the suanosine triphosphate-binding protein coupled receptor. The protein sequences shown in ADCR7618-ADCR7623 represent polymucleotide sequences related to the invention.
                                                                                                 GPCR; guanosine triphosphate-binding protein coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             guanosine triphosphate-binding protein coupled receptor; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynuclectide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of guanosine triphosphate-binding protein coupled receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 9; Le...
                                               Human GPCR related polynucleotide SEQ ID NO:2076,
                                                                                                                                                                                                                                                                                                                                                                                                                     (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY. (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Asai K, Akiyama Y, Aburatani H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 2076; 28pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADC87010 standard; DNA; 349999
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                                                                                                                                                                                                                                                                                                                         18-JUN-2002; 2002EP-00013517.
                                                                                                                                                                                                                                                                                                                                                                        18-JUN-2001; 2001JP-00246789
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-315783/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                       EP1270724-A2
                                                                                                                         gene therapy
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01-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48;
                                                                                            ds; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADC87010;
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Matches
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ADC87010/
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The invention relates to a novel polynucleotide encoding a guanosine triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of the invention may have a use in gene therapy. The polynucleotide and polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor. The polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
                                                                                                                                                                                                                                                                                                                                                                             New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 349999 BP; 91105 A; 78863 C; 81174 G; 98857 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 CCCGCCTCAGCTTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
NAT INST ADVANCED IND SCI & TECHNOLOGY.
CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.8%; Score 48; DB 9; Le
Local Similarity 100.0%; Pred. No. 9.9e-10;
tes 48; Conservative 0; Mismatches 0;
                                                                                                                                                Akiyama Y, Aburatani H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English
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20000US-0217487P

20000US-0218496P

20000US-022964P

20000US-02252113P

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2000US-0239937P
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2000US-0241785P.
2000US-0241787P.
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2000US-0241809P.
2000US-0241809P.
2000US-0241809P.
111-JUL-2000

26-JUL-2000

27-JUL-2000

28-JUL-2000

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20-OCT-2000; 2000US-0242521P 01-NOV-2000; 2000US-0244417P 08-NOV-2000; 2000US-0244417P 08-NOV-2000; 2000US-0244476P 08-NOV-2000; 2000US-0244477P 08-NOV-2000; 2000US-0246478P 08-NOV-2000; 2000US-0246523P 08-NOV-2000; 2000US-0246523P 08-NOV-2000; 2000US-0246523P 08-NOV-2000; 2000US-0246528P 08-NOV-2000; 2000US-0246528P 08-NOV-2000; 2000US-024651P 08-NOV-2000; 2000US-024661P 08-NOV-2000; 2000US-024661P 08-NOV-2000; 2000US-024661P 08-NOV-2000; 2000US-024661P 08-NOV-2000; 2000US-024661P 08-NOV-2000; 2000US-024661P 08-NOV-2000; 2000US-024661P 08-NOV-2000; 2000US-024661P 08-NOV-2000; 2000US-024661P 08-NOV-2000; 2000US-024661P 08-NOV-2000; 2000US-024651P 08-NOV-2000; 2000US-024921P 17-NOV-2000; 2000US-024921P 17-NO

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben

WPI; 2001-541565/60.

Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases.

Disclosure; SEQ ID NO 8137; 1701pp + Sequence Listing; English.

The invention relates to novel genes (ABA11004-ABA21534) and proteins CABB4678-ABB18001) useful for preventing, treating or ameliocating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,

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08-NOV-2000; 2000US-0246475P.
08-NOV-2000; 2000US-0246475P.
08-NOV-2000; 2000US-0246477P.
08-NOV-2000; 2000US-0246478P.
08-NOV-2000; 2000US-0246523P.
08-NOV-2000; 2000US-0246524P.
08-NOV-2000; 2000US-0246524P.
08-NOV-2000; 2000US-0246528P.
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08-NOV-2000; 2000US-0246528P.
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17-NOV-2000; 2000US-0246611P.
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2000US-0233063P.
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2000US-023937P.
2000US-0240960P.
               2000US-0227009F.
2000US-0228924F.
2000US-0229287F.
                                                   2000US-0229343P.
2000US-0229344P.
2000US-0229345P.
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20-0CT-2000; 2000US-024178787
20-0CT-2000; 2000US-02418988
20-0CT-2000; 2000US-024189898
20-0CT-2000; 2000US-02418269
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08-NOV-2000; 2000US-0246474P
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14-SEP-2000;
14-SEP-2000;
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29-SEP-2000;
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multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infectious. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                 Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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4.7%; Score 47; DB 5; Length 494;
Best Local Similarity 100.0%; Pred. No. 7.1e-09;
Matches 47; Conservative 0; Mismatches 0; Indels
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24-FEB-2000, 2000US-0180628P.
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14-AUG-2000, 2000US-021839P.
14-AUG-2000, 2000US-021818P.
14-AUG-2000, 2000US-022518P.
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14-AUG-2000; 2000US-0225268P.
14-AUG-2000; 2000US-0225270P.
14-AUG-2000; 2000US-0225447P.
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Human nervous system related polynucleotide SEQ ID NO 8135.

23-JAN-2002 (first entry)

ABA15804;

ABA15804 standard; DNA; 13160 BP

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AMX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
coctivity, and can be used in gene therapy and vaccine production. (I)
corrections and polymucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
complement the patients own production of (I). Additionally, (I)
coplymucleotides may be used to produce the secreted (I), by inserting the
complement the patients own production of (I). Additionally, (I)
coplymucleotides may be used to produce the secreted (I), by inserting the
complement and polymucleotides may be used to express the
complement and treat immune/haematopoietic-related diseases, especially
concerns and cancer metastases of haematopoietic-derived cells. AAK64703
concerns and cancer immune/haematopoietic antigen genomic
concerns and cancer immune/haematopoietic antigen genomic
concerns and cancer immune/haematopoietic antigen genomic
concerns complement invention. AAK849542 to AAK84950 and AAM82169
concerns and cancer invention. AAK84942 to AAK84950 and AAM82169
concerns and cancer invention. AAK84942 to AAK84950 and AAM82169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
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17-NOV-2000; 2000US-0249209P.
17-NOV-2000; 2000US-0249210P.
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17-NOV-2000; 2000US-0249214P.
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Human, nootropic, neuroprotective, cytostatic, dermatological, virucide, fimunosuppressive, antibiflammatory, anti-HIV; antibacterial, vulnerary, antiparkinsonian; antisickling; antianaemic; antiarthritic, cancer; antirheumatic, hepatotropic, cerebroprotective, antiinflammatory; antiallergic, antidiabetic, antiuloer; anticonvulsant; antifungal; antiparastic; cardiant; immune disorder, cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of by protein or gene therapy. The genes are isolated from a range of mutibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and covarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 8135; 1701pp + Sequence Listing; English.
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100.0%; Pred. No. 4.2e-09;
rative 0; Mismatches 0; Indels
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             01-DEC-2000; 2000US-0220391P.
01-DEC-2000; 2000US-0220391P.
05-DEC-2000; 2000US-0251160P.
05-DEC-2000; 2000US-02511988P.
06-DEC-2000; 2000US-0251988P.
06-DEC-2000; 2000US-0251856P.
08-DEC-2000; 2000US-0251866P.
08-DEC-2000; 2000US-0251866P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251989P.
                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
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                                           WO200159063-A2
                                                                                                                                   31 - JAN - 2000 | 24 - FEB - 2000 | 25 - MAR - 2000 | 26 - MAR - 2000 | 26 - MAR - 2000 | 26 - MAR - 2000 | 26 - MAR - 2000 | 27 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2000 | 28 - MAR - 2
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                 Homo sapiens
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Gaps

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Length 43419,

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The invention relates to a novel polynucleotide encoding a guanosine triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of the invention may have a use in gene therapy. The polynucleotide and polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor. The polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to novel carcinoma associated (CA) nucleic acid sequences from both mouse and human. In particular the invention discloses a recombinant nucleic acid comprising a fully defined PR domain protein II (PRDMI) - a carcinoma-associated gene) nucleotide sequence. The sequences of the invention are useful for identifying compounds that modulate the activity of a carcinoma associated protein (CAP) which are potentially useful in treating carcinomas. Among the diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel recombinant carcinoma-associated gene, PRDM11 useful for diagnosing cancer, and for screening for agents for treating cancers and
patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor.
                                                                                                                                                                                                                                                                                                                                             Sequence 43419 BP; 11054 A; 10220 C; 10281 G; 11764 T; 0 U; 100 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carcinoma associated gene; CA gene; PR domain protein 11; PRDM11; carcinoma associated protein; CAP; carcinoma; cancer; adenocarcinoma; breast cancer; inflammatory carcinoma; Paget's disease; aging; neurodegenerative disease; cytostatic; osteopathic; nootropic; neuroprotective; human; ds.
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                                                                                                                                                                                                                                                                                                                                                                                         4.7%; Score 47; DB 9; L. 100.0%; Pred. No. 3.4e-09; ive 0; Mismatches 0;
                                                                     Claim 1; SEQ ID NO 1451; 28pp; English
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2001US-00034650
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neurodegenerative diseases.
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ENGELHARD E K.
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20-DEC-2001;
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                                                                                                                                                                                                                                                                                               invention.
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                                                                                                                                                                                                                                                                               The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (art) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or uragenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune hyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
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                                                                                                                                         Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers
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                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 8136; 1701pp + Sequence Listing; English.
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100.0%; Pred. No. 4.2e-09;
tive 0; Mismatches 0; Indels
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CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
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                                                 Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human GPCR gene SEQ ID NO:1451
(HUMA-) HUMAN GENOME SCI INC.
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Les 47; Conservative
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                                              Barash SC,
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                                                                                                                                                                                            and metastases.
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RESULT 14 ADC86998,

ò 셤 New polynucleotide, useful for preparing a composition for treating a

WPI; 2003-315783/31. P-PSDB; ADC86999

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CC conditions that may be diagnosed or treated according to the invention

CC are cancers such as adenocarcinoma, breast cancer, inflammatory

CC carcinoma, Paget's disease, etc, aging, and neurodegenerative diseases.

CC The present sequence represents a CA nucleic acid sequence of the

XX Squence 63626 BP, 15622 A; 15444 C; 15753 G; 16795 T; 0 U; 12 Other;

Query Match

Query Match

Best Local Similarity 10.0%; Pred. No. 3.2e-09;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Search completed: July 10, 2004, 13:27:05 Job time: 501 secs

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Ties Bank (usp 5)

Scoring table:

Word size

Searched:

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Sequence:

OM nucleic -

en G

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USA

NIH-MCP Project URL: http://mgc.nci.nih.gov

Contact: MGC help desk

Email: cgapbs-remail.nih.gov

Tissue produrement: ATC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: MA.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford University School of Medicine, Stanford, CA 94305

Web site:
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1467)
Strausberg,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (01-NOV-2002) National Institutes of Health, Mammalian
Submitted (101-NOV), Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Homo sapiens, clone IMAGE:555526,
BC039500
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                     CD742581
BC447331
BC44687364
BM673564
BM673564
BM687366
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1 ggaattgttctcgaggccaa......aaaatgagcggccgcaagtt 990
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           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Database :

HIC 04-MAR-2003

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BC039500 BM980506 BU620427 BX406138

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760 691 1201 1467

56.8 37.4 34.6 34.4

343 343 343

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Query Match Length DB

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Description

N92133 Za23e12.rl BF820071 MR1-RT003 A0235733 HS_2015_B

BM679577 UI-E-EOD-BM679577 UI-E-EOD-BU64894 UI-E-ENI CD742581 UI-H-ET2-BU617331 UI-H-DF0-CA31312 UI-H-DF0-CA31312 UI-H-DF0-CA31312 UI-H-DF0-CA31312 UI-H-DF0-CA31312 UI-E-CQ1-BF509528 UI-H-EI4-BF509528 UI-H-EI4-BF509528 UI-H-EI4-BF3031002 Pan LTCG1-AM806113 Pan LTCG1-AM84113 RC5-CM001 AM84113 RC5-CM1 RC001

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                                                                                                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LiNL at: http://image.llnl.gov Series: IRAK Plate: 88 Row: g Column: 1
This clone has the following problem: retained intron.

Location/Qualifiers
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Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGATCTCCTGACCTCGTGATCCGCCCCCCCTCGGCTTCCCAAAGTGCTGGGATTACAGGCA
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/dev stage="Adult"
//dev stage="Adult"
//dev stage="DH10B (life Technologies) (Ti phage resistant)"
//clone lib="Ul-CF-ENI"
//note="Grgan: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
Ul-CF-ENI is a normalized cDNA library containing the
following tissue(s): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to
Bonalo, Lennon and Soares, Genome Research, 6:791-866,
1996. First strand CDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
CDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)1B tail. The
sequence tag for this library is CTGCTCAGGT.
TAG_TISSUB=Human Lung Epithelial Cell Lines untreated LPS
fh. 105 24
BM980506
UI-CF-EN1-add-a-08-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone
UI-CF-EN1-add-a-08-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 760)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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/clone="UI-CF-ENL-add-a-08-0-UI"
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Cells"
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Fax: 319 356 717
Email: paul-mccray@uiowa.edu
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99.4%; Pred. No. 0;
live 0; Mismatches 2;
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TAG LIB=UI-CF-EN1
TAG SEQ=CTGCTCAGGT"
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Seg primer: M13 FORWARD
POLYA=Yes.
                                                                                                                                 BM980506.1 GI:19602038
                                                                                                                                                                                                    (human)
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University of Iowa
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/Gragnism: Action Saptens:
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// (AD XTGE="Laxon:9506")
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Best Local Similarity 99.7%; Pred. No. 0;
Matches 393; Conservative 0; Mismatches 1; Indels C
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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bummalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 691)

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: James Martin

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, University of Iowa

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CLONE DISTRIBUTION: Clone distribution information can be obtained be pulmer: M13 FORWARD
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SOURCE
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REFERENCE

COMMENT

FEATURES

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Job Newton Road, 4156 MEBRF, Iowa City, IA 5242, USA Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seg primer: M13 Forward
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Organisms = minco sapieus.
/ Mol Lype="mRNA"
/ db_Xref="taxon:9606"
/ clone="UI=E-E00-aia-1-05-0-UI"
/ tissue type="fetal"
/ lab host="MHI0B (Life Technologies) (T1 phage resistant)"
/ lab host="MHI0B (Life Technologies) (T1 phage resistant)"
/ lone="Organ: eye; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR i; Site 2: Not I;
/ UI-E-EOO is a cDNA library containing the following tissue(s): fetal eye. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, e:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I; and cloned directionally into pT773-pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for the program; Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
                                                                                                                                           Eukaryofa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 669)
                                                                                                                                                                                                                                Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              458 ACGATTGGCCAGCGGGACTTAAGTGTTGTCTCTGAAGAGCATGGACATTAGTCTGGAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
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TAG TISSUE=human fetal eye
TAG LIB=UI-E-E00
TAG SEQ=CGCGTATACC"
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99.5%; Pred. No. 0;
                                                                                                                                                                                                                                                                                             Genome Res. 6 (9), 791-806 (1996) 97044477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                              BM679577.1 GI:18989473
                                                                                        Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="FETAL_LIVER"
/dev_stage="FETAL_LIVER"
/clone_lib="Homo sapiens FETAL_LIVER"
/note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecowy sites of the pCMVSPORT 6 vector. Library was not normalized."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCCCGAGGCCCAGGCCTCGCCGACCCGACTGCGCCTCCCGGTGGCCCCGCAGCGCCTT 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCGGTGGCCCTGGAGTGCAGGTCTTACCGTCCGAGATCGTCCGCAACTGGGCGAGCTGT 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        491 GCATGGGGCGTGGCTAAGGCCGTGGTTTGGTTACGATTGGCCAGCGGGACTTAAGTGTTG 432
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                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1201)
                                                                                                                                                                                                                 Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Bmail: sequefégenoscope.ns.fr. Web : www.genoscope.cns.fr
Library was constructed by life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8395.f For
Invitrogen. This sequence belongs to sequence cluster 8395.f For
http://www.genoscope.cns.fr/
sequence.ns.fr/
cgi-bin/cluster.cgirseq=cS0AM010CB10NP1&cluster=8395.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0AM010CB10NP1.
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Pred. No. 0;
0; Mismatches 1; Indels
                                                                                                       11, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGAAGGCTGTGTGCTTGAGGAGGCCCCGGCA 697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DM010YD19"
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99.7%;
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TAG_SEQ=CTGCTCAGGT"
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99.5%; Pred
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6hr_to LPS 24h
TAG_LIB=UI-CF-EN1
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Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                               GGGTGGGCCTTAGGGCGAAGGCGCAAACACCCCCGAAGTGGTTGTATACCGCAA
                                                                                                                                                           GATCCAGTGTGTGTGGGCTTTACAGGAAGAGCTCCACCTTCTCTGGAGTGTGCAGATG
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate
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Genome Res. 6 (9), 791-806 (1996)

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    /organism="Homo sapiens"

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/dev stage="Adult"
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//dev stage="Adult"
//dlob_host="DH10B (Life Technologies) (TI phage resistant)"
//clone_lib="UI-CF-EMI"
//note="Organ: Lung, Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-CF-EMI is a normalized CDMA library containing the
following tissue(s): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-866,
1996. First strand CDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an ECoR I adaptor, digested with Not
I, and cloned directionally into pT7T3-Pac vector. The
oligonuclectide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is CTGCTCAGGT.
TAG TISSUE=Hunan Lung Epithelial Cell Lines untreated LPS
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Pred. No. 0;
0; Mismatches 1;
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs.remail.inh.gov

Email: cgapbs.remail.inh.gov

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained

from Dr. M. Bento Soares, bento-soares@ulowa.edu

POLYA-Yes.
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                                           183 GGCCTTAGGGCGAGGCGCAGACACCCCGAAGTGGTTGGATTGTATACCGCAAGGGGC 324
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/none lib="NOI CASP DF0"
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP DF0 is a cDNA library containing the following tissue (s): Subchondral Bone. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996. First strand cDNA synthesis was primed
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NCI_CGAP_FT2 is a subtracted of CDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. TAG_LISUE-Human Lung Aveolar Macrophage
TAG_LISUE-Human Lung Aveolar Macrophage
TAG_LISUE-H-FT2
TAG_SEQ-GGCCATGCCG"
                                                                                                                                                                                                                          CD742581 623 bp mRNA linear EST 26-JUN-2003 UI-H-FT2-bjl-i-10-0-UI.81 NCI CGAP FT2 Homo sapiens cDNA clone UI-H-FT2-bjl-i-10-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
thtp://genome.uiowa.edu/distribution/cgap.html
Seq primer: M13 FORWARD
POLYA=Yes.
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/clone="UI-H-FT2-bj1-i-10-0-UI"
/tissue_type="Aveolar Macrophage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. 31.5%; Score 312; DB 14
Similarity 99.5%; Pred. No. 0;
02; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .623
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                  CD742581.1 GI:32293431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
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Best Local 9
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                                                                                                                                       RESULT 7
CD742581/c
                                                                                                                                                                                                                                                                     DEFINITION
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AUTHORS
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with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT713-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTTAAGCGTC.

TAG IISBUES-subchondral bone

TAG_ENG-GTTAAGCGTC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.inh.gov

Tissue Procurement: Dr. Jose Mercuende

CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained

from Dr. M. Bento Soares, bento-soares@uiowa.edu

POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BQ447041 628 bp mRNA linear EST 29-MAY-2002 UI-H-EUI-bac-p-06-0-UI.81 NCI CGAP_Ctl Homo sapiens cDNA clone UI-H-EUI-bac-p-06-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                             573
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGATCGTCCGCAACTGGGCGGAGCTGTGCATGGGGGCGTGGCTAAGGCCGTGGTTTGGTTA 458
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                                                                                                                                                                                                                                                                           Length 632;
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                                                                                                                                                                                                                                                                      Score 308; DB 13;
Pred. No. 0;
0; Mismatches 1;
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/organism="Homo sapie:
/mol_type="mRNA"
/db_xref="taxon:9606"
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BQ447041.1 GI:21250153
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99.7%;
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Homo sapiens
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                 358;
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Best Local Si
Matches 358;
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KEYWORDS
SOURCE
ORGANISM
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LOCUS
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGCCCTGGAGTGCAGGTCTTACCGTCCGAGATCGTCCGCAACTGGGCGAGCTGTGCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                     /tissue type="Osteoarthritic Cartilage"
/dev stage="Adult"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGATCACGCT.
TAG_TISSUE=osteoarthritic cartilage
TAG_LIB=UI-H-EU1
TAG_LSEQ=TGATCACGCT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 13;
/clone="UI-H-EU1-bac-p-06-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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0
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Pred. No. 0
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Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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CA313142.1
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Matches 32
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10. Caba http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP); Tumor Gene Index
Unpublished (1997)
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                                      153 TGATTTGGACCTGCGGGCCTCTGGACTTCCCTGATTCTCTGCTTGCATCTCCAGCAAGTC
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        TGATTTGGACCTGGGCCCTCTGGACTTCCCTGATTCTCTGCTTGCATCTCCAGCAAAGTC
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[lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
unknown library type
Insert Length: 966 Std Brror: 0.00
Seq primer: -40ml3 fwd. BT from Amersham
High quality sequence stop: 361.
Location/Qualifiers
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ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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AA687318.1 GI:2675509
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Homo sapiens
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University of lowa
University of lowa Med Labs, lowa City, IA 52242, USA
2024 University of lowa Med Labs, lowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of lowa
CDNA Library preparation. Dr. M. Bento Soares, University of lowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of lowa
DNA Sequencing by: Dr. M. Bento Soares, University of lowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbbosystems.com)
Seg primer: M13 FORWARD
POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/organism="Homo sapiens"
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/db xref="taxon:9606"
/clone=wlo-CP-FN0-aex-n-23-0-UI"
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/lab host="PullOB" (Life Technologies) (Tl phage resistant)"
/clone lib="WI-CF-FN0"
/note="Organ: Lung: Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UT FNO is a subtracted coll library defined from normalized Human lung epithelial cell libraries (ENI and DUI) The library was subtracted according to according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            818
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larity 99.3%; Pred. No. 0;
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/db_xref="taxon,9606"

/dlone="UT-E-CQ1-ada-e-09-0-UI"

/tissue type="Optic nerve"

/dev_stage="madult".

/dev_stage="madult".

/done="DH10B (Life Technologies) (T1 phage resistant)"

/lone=lib="UT-E-CQ1"

/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EccR I; Site 2: Not I; UT-E-CQ1 is a normalized CDNA library containing the following tissue(s): optic nerve. The library was constructed according to Bonaldo. Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BM687366 462 bp mRNA linear EST 28-FEB-2002 UI-E-CQ1-ada-e-09-0-UI.rl UI-E-CQ1 Homo sapiens cDNA clone UI.e-CQ1-ada-e-09-0-UI 5', mRNA sequence.
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Table 1319 315 8260

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1 (bases 1 to 46. Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene
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                                                                                             Length 300;
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0
                                                                                          Score 212; DB 12;
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                                                                                       Query Match 21.4%; Score 212; DB Best Local Similarity 100.0%; Pred. No. 0; Matches 212; Conservative 0; Mismatches
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Location/Qualifiers
         TAG_SEQ=CCATTAAGTG'
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Coordinated Laboratory for Computational Genomics
University of Iowa
This 19 335 956.

Fax: 319 335 956.

Fax: 319 335 956.

Fax: 319 335 956.

Fax: 319 335 956.

Thissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Scares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Scares, Univeristy of Iowa
CLONE Library Arrayed by: Dr. M. Bento Scares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Scares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
TGCATCTCCAGCAAAGTCCTGTCCCGTTGGCTTCATCCACTCTCTCACTTCTCTGC 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Homo. I (bases I to 300)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                    Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA sequence: 1-21, >AT_rich#Low_complexity (matched compliment) Seq primer: M13 Forward POLYA=Yes.
                                                                                                                                                                                                                                                                                                                 BM672504
300 bp mRNA linear EST 27-
UI-E-CQ1-ada-e-09-0-UI.sl UI-E-CQ1 Homo sapiens cDNA clone
UI-E-CQ1-ada-e-09-0-UI 3', mRNA sequence.
                                                                                                               Genome Res. 6 (9), 791-806 (1996)
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BM672504/c
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TITLE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CE I (bases 1 to 480)

RS NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

NACIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strain.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA iblary Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Www.bio.llnl.gov/bbrp/image/image.html
Seg primer: M13 Forward

POLYA=Yes.
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synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an BCOR I adaptor, digested with Not I, and cloned directionally into pTTT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the CAT18 tail. The sequence tag for this library is CCATTAAGTG. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
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/clone_lib="NCI_CGAP_Subs"
/note="Vector: pT7T3D_Pac (Pharmacia) with a modified
/note="Vector: pT7T3D_Pac (Pharmacia) with a modified
polylinker; Site_l: Not I, Site_2: Eco RI; NCI_CGAP_Subs
is a subtracted library derived from NCI_CGAP_Subs. The
NCI_CGAP_Subs library had 2.5 million recombinants. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGAGTGTGCAATGCGATCTAGGTGTGTCCACCCGATGGGAGCTGCGGGCCGGGCAAT
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/db_xref="taxon:9606"
/clone="IMAGE:3086731"
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BF509528/c
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single-stranded DNA preparation of NCI CGAP Subs was used as a tracer in a subtractive hybridization with a driver comprising; a pool of clones from NCI CGAP Subs (INAGE clone lds 273283-277415, 3068040-3065191; 25% of the driver population), a pool of clones from NCI CGAP Sub4 (INAGE clone lds 2723892-2773356; 25% of the driver population), NCI CGAP Sub6 (pool AIF-AJU, INAGE lds 2728969-2733190; 25% of the driver population), and NCI CGAP Sub6 (pool AIF-AJU, INAGE lds 30681864-3081850; 25% of the driver population). Subtraction was performed as previously described [Bonaho, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.

TAG_INSUE-LING

TAG_INSUE-LING

TAG_INSUE-LING

TAG_SEQ-GACAGC"
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NGT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
Seq primer: -40UP from Gibco.
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7g50h12.xl NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3309959 3',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 367)
NCI-CARP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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/mol type="mRNA"
/db xref="taxon:9606"
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/dev stage="adult"
//dev stage="adult"
//dev stage="adult"
//deb_host="DH10B"
//cloon=lib="MOXI_CGAP_PI28"
//note="Organ: Drostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NOT CGAP PI22 was prepared, and ss
circles were made in vitro. Following HAP purification
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the aame library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
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21.2%; Score 210; DB 10; Length 367;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 210; Conservative 0; Mismatches 0; Indels 0
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/clone="IMAGE:3309959"
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Search completed: July 10, 2004, 15:29:05 Job time : 3115 secs this Page Blank (Uspto)

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

escription	50 AC135050 44 AC135044	AC004975 Homo 8	AC118269 Homo s	14 ACII6914 HOMO B	AC011189 Homo 8	AL031848 Human	Z95116 Human DN	45 ACUU4645 HOMO 8 12 AL157412 Human	32 AF212832 Homo s	70 AC104070 Homo s	BX571818 Homo s	AC012440 Homo s	71 ACOSOSI FORO B	AC021165 Homo s	31 AC068301 Homo s	36 AC103706 Homo s	20011499 HOMO 8	AC103590 Homo s	AC013308 Homo s	55 AC016655 Homo 8	34 ACC27344 ACCC B	19 AC010419 Homo s	53 AC092463 HOMO 8	AC013637 AOMO 8	AC004524 Homo s	45 AC106045 Homo s	64 AC009964 Homo s	AC004555 HOMO S	AC093029 Homo 8	73 AC092473 Homo s	AC074268 Homo s	25 AC1266325 HOMO 8	AC004890 Homo B	70 AC007570 Homo s	BX640519 Human	23 BX572623 HOMO 8	SE LA MARCEL	0 bp DNA linear PRI 27-FEB-200 clone RPI1-196G11, complete sequence.			a; Craniata; Vertebrata; Eute	s; Catarrhini; Hominidae; Homo.	Stanford Human Genome Center and Los	
B ID	200	AC0049	AC1182	ACITES	AC0111	HS2020	HS57G9	AC0046	AF2128	AC1040	BX5718	AC0124	ACOSOS	AC0211	AC0683	AC1037	AC0061	AC1035	AC0133	ACOLEG	AC0935	AC0104	AC0924	ACO136	AC0045	AC1060	AC0094	AC0048	AC0930	AC0924	AC0742	AC0263	AC0048	AC0075	BX6405	BX5726	A1,T4	8223 16	70306	â	nordat	imate	nstitute, boratory.	
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98559 CTGTGTGTGAGGAGGCCCCGCAGATCCAGTGTGTGTGTTTACAGGAAAGAGCT 98618
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Consensus quality: 18638 bases at least 030
Consensus quality: 188095 bases at least 030
Consensus quality: 188095 bases at least 030
Estimated insert size: 1700000; agarose-fp estimation
Estimated insert size: 1700000; agarose-fp estimation
Quality coverage: 6.7 in 020 bases; sum-of-contigs estimation.
* NOTE: This is a "working draft" sequence. It currently
* consists of 22 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Catarrhini, Hominidae, Homo.
                                CTGTGTGTGGCTGAGGAGGGCCCGGCA-ATCCAGTGTGTGTGGGGCTTTACAGGAAAGAGCT
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1302: gap of unknown length
2468: contig of 1166 bp in length
2568: gap of unknown length
4077: contig of 1509 bp in length
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AC135044.1 GI:23505535
HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
Homo sapiens (human)
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Mammalia, Eutheria, Primates, Catarr
1 (bases 1 to 195476)
DOB Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
2 (bases 1 to 195476)
DOB Joint Genome Institute.
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Center clone name: CITB-E1_2551B20
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                                                                                                                                                                                                                                                                                                                               Submitted (27-FBB-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Feb 27, 2003 this sequence version replaced gi:24211094. Draft Sequence Produced by DOE Joint Genome Institute www.jgi.dee.gov Finishing Completed at Stanford Human Genome Center and Los Alamos National Laboratory www.shgo.stanford.edu Quality: Phrap Quality >40 99.7% of Sequence; Estimated Total Number of Errors is 0.3.
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                                                                                              Submitted (05-OCT-2002) Production Sequencing Facility, DOB Joint denome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA (bases 1 to 182230)

DOB Joint Genome Institute.
                                                                                                                                                                                        Direct Submission
Submitted (22-OCT-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 18220)
DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
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/mol type="genomic DNA"
/db_xref="texon:9606"
/chromosome="16"
/clone="RP11-196G11"
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Direct Submission
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106667 CTAAGGCCGTGGTTTGGTTAGGCCAGCGGGACTTAAGTGTTGTCTCTGAAGACA 106726
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                                                                                                                                                                                                                                                                    AC004975 96975 bp DNA linear PRI 21-DEC-1999
Homo sapiens PAC clone RP5-1142019 from 7q35-q36, complete
sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (12-JUN-1998) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
Mo 53108, USA
4 (bases 1 to 96975)
Waterston, R.H.
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Park Avenue, St. Louis, Missouri 63108, USA
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Submitted (05-MAY-1999) Genome Sequencing Center, Washington
Inversity School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 96975)
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Catarrhini, Hominidae, Homo.
                                                                                              559 AGGICTAGGAAGCGGGTGTGGGGTGGGGCCTTAGGGCCGAGGCGCAGACATACCCCGAAGTG
                                                                                                                                                                                                                                             GTTGGATTGTATACCGCAAGGGGCTGGATCGAACCCCCCCAAAGACACTGGGAAGGCTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 96975)
Leonard, S. and Strowmatt, C.
The sequence of Homo sapiens PAC clone RP5-1142019
Unpublished
3 (bases 1 to 96975)
Waterston, R.H.
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Contact: sapiens@watson.wustl.edu
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Mammalia, Eutheria, Primates, Catarrhini
1 (bases 1 to 96975)
Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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                                                                                                                                                                                                                                                                                                                                    679 GGCTGAGGAGGCCCGGCA 697
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Submitted (27-AUG-1999)
University, 4444 Forest
6 (bases 1 to 96975)
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Homo sapiens
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Pred. No. 3.2e-272;
0; Mismatches 1; Indels 0;
    4177: gap of unknown length 5572: contrig of 1595 bp in length 5572: contrig of 1850 bp in length 7722: contrig of 1850 bp in length 7722: contrig of unknown length 1852: gap of unknown length 9059 11051: gap of unknown length 11052 1161: gap of unknown length 11052 1161: gap of unknown length 11052 13641: contrig of 1939 bp in length 11052 13641: contrig of 1939 bp in length 13742 1738: gap of unknown length 1739 22030: contrig of 4920 bp in length 1739 17002: contrig of 4972 bp in length 1739 17002: gap of unknown length 17003 17102: gap of unknown length 17003 1721: contrig of 1251 bp in length 17003 1722: gap of unknown length 17003 1722: gap of unknown length 17003 1720: gap of unknown length 17003 1720: gap of unknown length 17003 17003: contrig of 12545 bp in length 17003 17003: gap of unknown length 17003 17003: gap of unknown length 17003 17003: gap of unknown length 17003 17003: gap of unknown length 17003 17003: contrig of 12045 bp in length 17003 17003: contrig of 12040 bp in length 17003 17003: contrig of 12040 bp in length 17003 17003: contrig of 12004 bp in length 17003 17003: contrig of 12003 bp in length 17003: contrig of 12003 bp in length 17003: contrig of 12003 bp in length 17003: contrig of 12003 bp in length 17003 17003: contrig of 12003 bp in length 17003: contrig of 12003 bp in length 17003: contrig of 12003 bp in length 17003: contrig of 12003 bp in length 17003 17003: contrig of 12003 bp in length 17003 17003: contrig of 12003 bp in length 17003 17003: contrig of 12003 bp in length 17003 17003: contrig of 12003 bp in length 17003 17003 bp 
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Organism=Homo sapiens"

/mol type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="lch"

/clone="CTD-2551B20"

/clone_lib="CalTech human BAC library D"
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Matches 558; Conservative
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repears; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GHR7, send mailto:egreen@nhgri.nih.gov/ or see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The library is from This clone was derived from human PAC library RPCI-5, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is fro

one male donor.

The clone may be obtained either from Genome Systems, Inc (http://www.genomesystems.com) or Research Genetics, Inc. (http://www.resgen.com); or from Pieter de Jong.

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the right is RP4-814D15. Actual start of
this clone is at base position 1 of RP5-1142J19; actual end is at
base position 96975 of RP5-1142J19.

transposon was identified in the cloning vector for RP5-1142J19. Location/Qualifiers
1. .96975

/organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" source FEATURES

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3325. .3883 /rpt_family="Retroviral" rpt_family=" (CAAAA) n" /rpt_family="Alu" 3325. .3883 /rpt_family="L1" .3190 repeat_region repeat_region

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Direct Submission

Bubmitted (21-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Gbases 1 to 129788)

Birren, B. Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Changlan, C., Camporlano, A., Chang, J., Changlan, J., Camporlano, A., Chang, J., Changel, Y., Colangel, N., Collins, S., Collymore, A., Chang, J., Chang, J., Candra, J., Candra, J., Candra, J., Candra, J., Candra, J., Cardyna, S., Ginde, S., Gord, S., Goyette, M., Gage, D., Farreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Gand-Pierre, N., Hagos, B., Hotton, L., Hulme, W., Ilav, I., Gardyna, C., Kanata, A., Kells, C., Landcra, F., Madchan, C., Madchan, C., Madchan, P., Marchis, C., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Inu, G., MacLean, C., MacMan, P., McKartas, A., Kells, C., Ladocque, K., Mathova, T., Meran, P., McKartas, A., Kells, C., Ladocque, K., Mathova, T., Meran, R., Marquis, N., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers,
       O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,N., Schauer,S., Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
Center project name: 126202
Center clone name: 2383_D_6
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|mol_type="genomic DNA"
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complement(2..224)
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complement(365..413)
/rpt_family="L2"
415..546
/rpt_family="L2"
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649
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/rpt_family="AluSp"
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Homo sapiens chromosome 17, clone CTD-2383D6, complete sequence.
AC118269
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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15076. .15380
/rpt_family="Alu"
                                                                                                                                          Score 79;
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CE [bases 1 to 18856]

Birren, B. Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Eloom, T., Boguslavkiy, L., Anderson, S., Brown, A., Camaraca, J., Campoplano, N., Changalter, B., Choepel, Y., Colangelo, M., Contins, S., Collymore, A., Cooke, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Garbam, L., Grand-Pierre, N., Cooke, J., Marchas, R., Karatas, A., Karatas, A., Kalls, C., LaRocque, K., Lindhason, R., Lindhason, R., Lindhason, R., Macthews, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Macdonald, P., Major, J., Maylor, J., Ngyken, C., Nicol, R., Murphy, T., Naylor, J., Ngyken, C., Nicol, R., Murphy, T., Naylor, J., Ngyken, C., Nicol, R., Murphy, T., Naylor, J., Ngyken, C., Nicol, R., Spencer, B., Stender, S., Schubers, S. 95562 CGATCTCCTGACCTCGTGATCCGCCCCCCTCAGCTTCCCAAAGTGCTGGGATTACAGGCA 95503 AC116914 138536 bp DNA linear PRI 06-AUG-2002 Homo sapiens chromosome 17, clone CTD-319515, complete sequence. AC116914 ö Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [1 (bases 1 to 138536)]
Birren, B., Nusbaum, C. and Lander, E. Homo sapiens chromosome 17, clone CTD-319515 34 CGATCTCCTGACCTCGTGATCCGCCCCCCCTCCCAAAGTGCTGGGATTACAGGCA 93 Gaps . 0 Length 129758; 0; Indels Query Match
6.7%; Score 66; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 3.5e-25;
Matches 66; Conservative 0; Mismatches 0; AC116914.5 GI:22038652 Homo sapiens (human) 95502 TGAGCC 95497 Homo sapiens 94 TGAGCC 99 Unpublished RESULT 5 AC116914/c LOCUS KEYWORDS SOURCE ORGANISM DEFINITION REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS ACCESSION VERSION B ઠે Вþ

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clone_lib="CITD2 Human BAC'
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/rpt_family="Aludb"
complement(15699. .16011)
/rpt_family="Aludo"
complement(16152. .16196)
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complement(14154..14464)
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complement(15023..15320)
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complement(8667, .8963)
/rpt_family="Alusc"
10023, .1000
                                                                                                   /rpt_family="Aluub"
complement(1109. .1343)
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/rpt_family="Alusc"
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y="L2"
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5084. 5389
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complement (6125. .6286)
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975. .7000
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3941. .4060
                                                                                                                                                                                                                 rpt_family="Charlie4a"
215. .2517
                               complement (240. .399)
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complement (400. .691)
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complement (692. .833)
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583. .4895
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2082..12156
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omplement(8377. .
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Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Straus, N., Shiramanian, Tadas, T., Talagaio, J., Vasasilacv, H., Vasasilacv, Travers, M., Travis, N., Trigilio, J., Vasasilacv, H., Vasasilacv, H., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., W
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Center: Whitehead Institute/ MIT Center for Genome Research
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Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
.----- Project Information
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Center clone name: 3195_I_S
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6.7%; Score 66; DB 9; Length 138536; 100.0%; Pred. No. 3.5e-25;

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AC011189.7 GI:14595908
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Matches 66; Conserva
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Direct Submission

L. Submitted (03-007-1997) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 21, 1998 this sequence version replaced gi:2978483.

All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                          111268 CGATCTCCTGACCTCGTGATCCGCCCCCCCCTCCCCAAAGTGCTGGGATTACAGGCA 111209
     ö
                                                                                                                                                                                                                                                                                                                AC002993 140210 bp DNA linear HTG 21-MAR-1998
Homo sapiens chromosome 17 clone HCIT169H9 map 17, *** SEQUENCING
IN PROGRESS ***, 6 unordered pieces.
                                                93
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Birren, B., Fasman, K., McKernan, K., Nusbaum, C., Richardson, P. and
                                                34 CGATCTCCTGACCTCGTGATCCGCCCCCTCAGCTTCCCAAAGTGCTGGGATTACAGGCA
     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://ftp.genome.washington.edu/RM/RepeatMasker.html.
*NOTE: This is a 'working draft' sequence. It currently
consists of connigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* trus of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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Organism="Homo sapiens"

(mol_type="genomic DNA"

/db_xref="taxon:9606"

/mcp="17"
/map="17"
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Center of the name: 1487

Center come name: 231G16

Sequencing vector: Plasmid; 104; 14 of reads
Sequencing vector: Plasmid; 10875; 4% of reads
Sequencing vector: Plasmid; 10875; 4% of reads
Sequencing vector: Plasmid; 104; 55% of reads
Chemistry: Dye-primer-amersham; 8% of reads
Chemistry: Dye-primer-amersham; 8% of reads
Chemistry: Dye-primer-amersham; 8% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 203261 bases at least Q40
Consensus quality: 203261 bases at least Q30
Consensus quality: 207122 bases at least Q30
Insert size: 177000; agarose-fp
Insert size: 177000; agarose-fp
Insert size: 208485; su.
* NOTE: This is a "working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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contigo of 9341 bp in length

contigo of 15930 bp in length

gap of 100 bp

contig of 27812 bp in length

gap of 100 bp

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contigo of 64921 bp in length

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contigo of 64921 bp in length
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Contact: sequence_submissions@genome.wi.mit.edu
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181394 CGATCTCCTGACCTCGTGATCCGCCCCCCCCCAGCTTCCCAAAGTGCTGGGATTACAGGCA 181453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 CGATCTCCTGACCTCGTGATCCGCCCCCCTCAGCTTCCCAAAGTGCTGGGATTACAGGCA 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL031848.11 GI:4914512
HTG; Acyl Coenzyme A Thioester Hydrolase; Ank repeat; Brain
Acyl-CoA Hydrolase; Enhacer of Split; Espin; Hairy; HBACH; HES2.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 143065)
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/clone_lib="RPCI-11 Human Male BAC"
1. .2927
/note="asembly_fragment
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Pred. No. 3.6e-25;
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/note="assembly_fragment"
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138672. .209885
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rat Espin LIKE protein

COMMENT

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SPVIVWLVSCTDVSLSRQDKÄGATAMHFAASRÄHTKVLSWLLLHGGE1SADLMGGTPL
HDAAENGELECCQILVVNGAELDVRDRDGYTAADLSDFNGHSHCTRYLRTVENLSVEH
RVLSRDPSAELEAKQPDSGMSSPNTTVSVQPLNFDLSSPTSTLSNYDSCSSSHSSIKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OHPPCGLSSARAADTQSYMDMINPELGLPRGTIGKFTPPPPPPPPPPPPPGTQLPP
PPPCYPARPORPOADADIYMQTKWKLRHVBTFSALKKELSSCOGHOGHORRQDSSRKPR
AFEKQPSTGDYYRQIGRCPGETLAARPGMAASEEAALLPGNHYPNGCAADPKASRELP
PPPPPPPPPLDEAASSPPPAPPLLESAGPGCGQRRSSSSTGSTKSFNMMSPTGDNSB
                                                                                                                                                                                                                                                                            /tränslation="Malegalgaarggeldvirslhaagligeslrdpeldalpvhhaa
Regkhichretybebalpaararangarpahnaarafehlacigmilsgegervordn
Sgatvillarreghebvynvilhhgggdptaatdmgalp inyaakgdppslelivel
Ypegvnagtrogatplylacgeghlevtgylvgeggadpharahdgmtplhaaagmg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLAEIKAGKSLKPTPQSKGLTTVFSGIGQPAFQPDSPLPSVSPALSPVRSPTPPAAGF
QPLLNGSLVPVPPTTPAPGVQLDVEALIPTHDEQGRPIPEWKRQVMVRKMQLKYQEEE
                                /note="match: proteins: Tr:Q63618 Tr:Q24341 Tr:O89019
Sw:Q01484 Tr:Q17343 Sw:Q01485 Tr:Q25338 Tr:Q2625"
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/note="AluSq repeat: matches 1. .299 of consensus"
/note="AluSc repeat: matches 1. .300 of consensus"
10241. .10539
/note="AluSc repeat: matches 1. .294 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="MIR repeat: matches 100. .244 of consensus"
15679. .15715
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3220. ,13427
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/note="WIR repeat: matches 31. 162 of consensus"
9640. 9931
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14376. .14517
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/note="MIR repeat: matches 57. .121 of consensus"
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/note="L1M3e repeat: matches -370. .12 of
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/note="3_copies 23 mer 81% conserved"
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/note="4_copies 45 mer 68% conserved"
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/note="MIR repeat: matches 173.
11758. .12719
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/note="L2 repeat: matches 2414.
13434, .13624
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                                                                                                                                                           .1 (novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'evidence_not_experimental
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'evidence=not_experimental
12259. .12372
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/product="dJ20208.1 (novel
                                                                                                                                                                                 containing Ank repeats)"
/protein_id="CAB46197.1"
/db_xref="G1:5327035"
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2810. .13093
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/note="CpG island"
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'note="CpG island"
gene="dJ20208.1"
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7708.
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                                                                                                                                                                                                 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with ris sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with thair source databases:

Em:, EMBL: Sw.: SWISSROT; Tr:, TREMBL: Wp:, WORNPEP; Information on the WORNPEP database can be found at the work anger ac.uk/Projects/C_elegans/wormpep This sequence chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at the chromosome 1 mapping Group. Further information can be found at the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the pla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is the entire insert of clone RP1-20208 The true left end of clone RP1-120G22 is at 135606 in this sequence. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /evidence=not experimental
complement(join(<732. .995,1080. .1225,3737. .3935,
4026. .4187,6893. .7164,8146. .8347,11763. .11894,
12020. .12202,12388. .12574,24409. .24602,27579. .27872))
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/note="Alusg/x repeat: matches 83..309 of consensus"
/note="match: 635..907)
/note="match: 635..907)
/note="match: 635..895)
/note="match: 635..895)
/note="match: 635..895)
/note="match: 635..895)
/note="match: 635..897)
/gene="dJ20208.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .144 of consensus"
   On May 28, 1999 this sequence version replaced gi:4678811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/db_xref="RZPD:RPCIP704008202"
/db_xref="taxon:9606"
/chromcosome="l"
/map="p36.11-36.31"
/clone="RP1-20208"
                                                   Center: Wellcome Trust Sanger Institute
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note="MIR repeat: matches 13.
                                                                                                                       Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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FEATURES

consensus

conserved" conserved" .2615 of consensus"

conserved"

gene mRNA

CDS

.189 of consensus" .306 of consensus"

consensus,

.261 of

us-09-972-032-1.rge

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regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 10); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

This sequence was generated from part of bacterial clone contigs of human chromosome 22.

Mapping Group. Further information can be found at http:/www.sanger.ac.uk/HGP/Chr22

This sequence is the entire insert of clone CTA-57G9 The true right end of clone RPS-11779 is at 100 in this sequence.
     Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the Workner database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep CTA-57G9 is from the human BAC library described in U-J. Kim et al. (1996) Genomics
                                                                                                                                                                                                                                                                                                     This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="13.6 copies 40 mer
AGAGGTGATGAAGAACAGGGAGAGGGAGAGGGTGATGA 780% conserved"
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1177. .1188
/note="2.0 copies 6 mer GAAAGG 24% conserved"
complement (1326. .1866)
/note="MITIF2 repeat: matches 33. .554 of consensus"
complement (1867. .2202)
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/note="FLAM C repeat: matches 1. .129 of consensus"
complement (2660. .3073)
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/note="2.0 copies 6 mer GCCATG 24% conserved"
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complement(105. .682)
/note="match: GSS: Em:B14096"
complement(387. .678)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="13.0 copies 2 mer GT 43% conserved"
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/note="14.0 copies 1 mer T 28% conserved"
4615. .4629
                                                                                                                                                                              Center: Wellcome Trust Sanger Institute
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//note="match: GSS: Em:B14098"

complement (430. .682)

/note="match: GSS: Em:B36168"
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/note="match: GSS: Em:B14225"
                                                                                                                                                                                                                            Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="22"
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                                                                                                34, 213-218.
VECTOR: pBAC108L
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Direct Submission
Direct Submission
Direct Submission
Submitted (05-70N-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
Numquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on Feb 5, 1998 this sequence version replaced gils5nlate.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HBS /G9 113872 bp DNA linear PRI 05-JUN-2003 Human DNA sequence from clone CTA-57G9 on chromosome 22q12.1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 113872)
                                                                                                                                                                                                                                                                                                                     9202. 19370
'note="AluSg/x repeat: matches 134. 302 of consensus"
19372. 19665 ------ 793 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 TOCTGACCTCGTGATCCGCCCCGCCTCAGCTTCCCAAAGTGCTGGGATTACAGGCATGAGC
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note="L2 repeat: matches 2593. .2706 of consensus"
1016. .21075
                                                                                                                                                                                                                                                                 18925. .19128

// Anote="12 repeat: matches 2324. .2555 of consensus"

19202. .19370
                                                                                                                                                                                                     .2605 of consensus"
                                                   .311 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                              note="MIR repeat: matches 218. .254 of consensus" 16339. .16334 note="Aludo repeat: matches 18. .311 of consensus'
                                                                                                                                                                                                                                                    note="AluSx repeat: matches 1. .291 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21171. .21501
/note="AluSx repeat: matches 1. .311 of consensus"
22030. .22214
                                                                                                     .261 of consensus"
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100.0%; Pred. No. 1.7e-23;
ative 0; Mismatches 0;
                                                                                                                                              note="MIR repeat: matches 130.
                                                                                                  'note="MIR repeat: matches 32.
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complement(20501. .20541)
/gene="dJ20208.1"
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Z95116.1 GI:2832592
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Best Local Similarity
Matches 63; Conserv
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KEYWORDS
SOURCE
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GI:3097839
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AC004645/c
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KEYWORDS
                                                                                              . >22209)
                                                                                                                                                                                                                                                                                                                                                                                                              /evidence=not_experimental
produce=nbk5709.1 (novel Kringle and CUB domain protein)"
/protein_id="CAB62952.1"
/db_xref="GI:6572252"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAMSSVVYSPDFPDTYATGRVCYWTIRVPGASHIHFSFPLFDIRDSADMVELLDGYTH
RVLARFHGRSRPPLSFNVSLDFVILYFFSDRINQAQGFAVLYQAVKBELPQERPAVNQ
TVAEVITEQANLSVSAARSSKVLYVITTS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="PGNLGCYKDHGNPPPLTGTSKTSNKLTIQTCISFCRSQRFKFAG
MESGYACFCGNNPDYWKYGEAASTECNSVCFGDHTQPCGGDGRIILFDTLVGACGGNY
/note="3.0 copies 5 mer CAAAA 21% conserved"
join(4811. .4935,8717. .8870,20796. .21128,22078. .22209)
/gene="bK5769.1"
join(4811. .4935,8717. .8870,20796. .21128,22078. .>22206
/gene="bK5769.1"
/gene="bK5769.1"
match: ESTE: Em:AA506741 Em:Aa670682
match: proteins: Tr:P91972 Sw:P98065 Tr:Q15113 Tr:O35113
Tr:Q2413 Tr:O7764 Tr:O7763 Tr:O8204 Sw:P97435
Tr:O60494 Tr:O77674 Tr:O77674 Tr:O86689
Tr:O60494 Sw:P978066 Tr:O75074 Tr:O8689
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note="Tigger5 repeat: matches 2307. .2406 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="LiME1 repeat: matches 5043. .5827 of consensus" 5112. .6420
for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a for a
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//note="AluSg/x repeat: matches 83. .296 of consensus"

11123. .11661

//note="LIMB7 repeat: matches 5583. .6122 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12663. .12810
/note="AluSg/x repeat: matches 139. .290 of consensus"
complement(1352. .13690)
/note="Mix repeat: matches 78. .252 of consensus"
complement(13684. .13732)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               502. .6965
note="LIME1 repeat: matches 4987. .5467 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            273. .7946
note="LiME1 repeat: matches 5467. .6068 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1247. .8291
.hote="LIME1 repeat: matches 6068. .6113 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .6184 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9327. 8426
Note="MIR repeat: matches 134. .262 of consensus"
8941. .8952
/note="3.0 copies 4 mer CCCT 24% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9570. .9582
//note="13.0 copies 1 mer A 26% conserved"
complement(9708. .10119)
//note="ML/IIC repeat: matches 8. .465 of consensus"
complement(10556. .10724)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       966. .7272
'note="AluSx repeat: matches 3. .311 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .300 of consensus"
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/note="2.1 copies 9 mer TTAAAATGG 38% conserved"
complement(12111. .12286)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4995. .5311
/note="LiMB7 repeat: matches 5850.
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AC004645 44174 bp DNA linear PRI 01-MAY-1998 Homo sapiens chromosome 16, cosmid clone 400C4 (LANL), complete
                                                                                                                                                                                                                                                                                                                                                                                         consensus
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(bases 1 to 44174)

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(conse, n. buckingham, J., Chasteen, L., Thompson, S., Goodwin, L., Bryant, J., Tesmer, J., Meincke, L., Longmire, J., White, S., Tetum, O., Campbell, C., Fawcett, J., Maltbie, M., Misra, M. and Deaven, L.

(consequencing of Human Chromosome 16pl3.3
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Direct Submission
Submitted (01-MAY-1998) Center for Human Genome Studies, DOE Joint Genome Institute, Los Alamos National Laboratory, MS M888, Los
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Link1 repeat: matches 6659. .6744 of consensus"
complement(15320. .15625)
/note="AluSp repeat: matches 1. .307 of consensus"
complement(15626. .16420)
/note="Link1 repeat: matches 5869. .6659 of consensus"
16421. .16729
                                                                                                                                                                                                                                                                                                                                                                                   15158. .15230
/note="L1MCa repeat: matches 1995. .2064 of consensus"
complement(15233. .15319)
                                                                                                                                                                                                                              complement(14788. .14982)
/note="LIME1 repeat: matches 6741. .6952 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
/note="L2 repeat: matches 3182. .3229 of consensus" complement (13805. .13964)
                                                                      'note="MER104 repeat: matches 1. .176 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="AluY repeat: matches 1. .309 of consensus"
                                                                                                                                                              complement(14535..14785)
/note="MIR_repeat: matches 5..259 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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                                                                                                                                                                                                                                                                                    14983. 15002
/note="10.0 copies 2 mer TA 40% conserved"
15003. 15057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 60; DB 9; Le
Pred. No. 7.8e-22;
                                                                                                                                /note="2.3 copies 7 mer GTTTAAG complement(14535. .14785)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pred. No. 7.8 tive 0; Mismatches
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9238. .....y="Alu"

pote="GRAIL 2 excellent exon, frame 1"

complement(10614. .10716)

/note="GRAIL 2 excellent exon, frame 2"

complement(11928. .12071)

/rpt family="Alu"

13214. .1354^
                                                                                                                                                                                                                                                                                                                                                                       note="GRAIL 2 excellent exon, frame 2"
note="GRAIL 2 excellent exon, frame 0"
note="GRAIL 2 excellent exon, frame 0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="99% identity BST zj31a04.sl"
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IMPORTANT: This sequence is not the entire insert of clone RP11-125P18 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP5-1097P24 is at 45355 in this sequence. The true right end of clone RP5-1185K9 is at 100 in this
                 For
                 Pieter de Jong.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       consensus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             831. .966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 koswell Park Cancer Institute by the group of Piet further details see http://bacpac.med.buffalo.edu/
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complement (3402. .3545)
/note="match: STS: Em:G08408"
complement (3428. .3580)
/note="match: GSS: Bm:AL236234"
complement (3452. .3586)
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//note="26 copies 4 mer atgg 778
complement (3375. .3539)
/note="match: GSS: Em:AL185783"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (3139, .3392)
/note="match: GSS: Em:AQ388774"
complement (3200, .3582)
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/note="match: GSS: Em:AQ972678"
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//note==march: 68S: Em.AAL241313"
complement (3340. .3582)
/note==march: 6SS: Em.AQ348189"
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/note="match: STS: Em:AU029014"
3351. .3580
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3371. .3474
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/note="match: GSS: Em:AL273514"
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/note="match: STS: Em:AU024971"
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/note="match: GSS: Em:AQ727438"
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/hote="match: GSS: Em:AL285765"
3360. .3534
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                                                                                                                                                                                                                                                         1. .45454
/organism="Homo sapiens"
                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (638.
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Submitted (27-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire,
CENO 15A, UK. Emaile mquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Jul 1, 2000 this sequence version replaced gi:8546617.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
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Emm:, EMBL; Sw:, SWISSPRCT; Tr:, TREMBL; Wp:, WGRMPEP; Information on the WORNPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at Mttp://www.sanger.ac.uk/RgY/Chr20 Rpping Group. Further information can be found at RPII-125P18 is from the library RPCI-11.1 constructed at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL157412 45454 bp DNA linear PRI 31-JUL-2000 Human DNA sequence from clone RPI1-125P18 on chromosome 20 Contains STSs and GSSs, complete sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 45454)
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complement(35186, .35517)
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37067, .37493
                                                                                                            / romplement (34043. .34190)
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complement (34498. .34794)
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                                                                     complement (33411. .33770)
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17452. .38121
                        complement (33104.
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37923. .37945
/note="(A)23"
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'rpt_unit="T"
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                                                                                                                                                                                                                                                                                                     .35210
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note="(T)27"
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REFERENCE

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KEYWORDS VERSION

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AF212832.5 GI:25100909
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// note="11M4 repeat: matches 2765, .3567 of consensus" 26138 . .26440
// note="%12640 repeat: matches 1. .295 of consensus" 26411. .26763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="Alusx repeat: matches 1. .307 of consensus" (442. 16595)
Thote="MERSA repeat: matches 9. .189 of consensus" 8358. .18757
Note="Limc3 repeat: matches 7324. .7733 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="LIME1 repeat: matches 5708. .6158 of consensus" 1283. .22286 note="LIME1 repeat: matches 4597. .5629 of consensus"
                                                                                                                                                                                                                                                                                              .514 of consensus"
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// Ancte="match: GSS: Bm:AQ184417"
// Ancte="match: GSS: Bm:AQ184417"
// Ancte="MIX repeat: matches 31. .197 of consensus"
// Ancte="WIRESA repeat: matches 64. .168 of consensus"
// Ancte="WIRESA repeat: matches 1. .224 of consensus"
// Ancte="WIRESA repeat: matches 1. .224 of consensus"
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// Ancte="WIRESA repeat: matches 1. .224 of consensus"
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                                                                                                                                                                       5509, .5689
note="MERSA repeat: matches 1. .186 of consensus"
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note="MER5A repeat: matches 1. .189 of consensus"
3779. .13845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="MERSA repeat: matches 5. ,71 of consensus" 3917. .14215
note="Alusx repeat: matches 1. ,299 of consensus" 6015. .16486
note="match: GSS: Em:AQ147161" 6019. .16319
                                                                                                                                                                                                                            .228 of consensus"
                                                                                                                                                                                                                                                                                                                                                                         8426. .8473
/note="12 copies 4 mer gaag 85% conserved"
9612. .9679
/note="12 copies 4 mer tata 81% conserved"
9678. .9719
/note="21 copies 2 mer at 83% conserved"
                                 3490. .3581
/note="23 copies 4 mer tgga 84% conserved"
3581. .3932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     684. .9719 note="9 copies 4 mer atat 88% conserved"
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700ce="match: STS: Bm:HSPF12G6"
7696. 7990
7note="LTR33 repeat: matches 172.
                                                                              /note="THELA repeat: matches 1.
complement(4751. .5369)
/note="match: GSS: Em:B53127"
                                                                                                                                                                                                                                                                                                           7980. .8562
/note="match: GSS: Em:AQ535194"
7986. .8542
/note="match: GSS: Em:AQ548736"
                                                                                                                                    complement (5089. .5368)
/note="match: GSS: Em:AQ242433"
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/note="MIR_repeat: matches 46.
                note="match: GSS: Em:AL276849"
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Direct Submission

Signature of Molecular Direct Submission

Loughtted (08-DEC-1999) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany

Direct Submission

Submitted (08-DEC-1999) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany

Signatur, D. and Plazzer, M.

Direct Submission

Loughmitted (10-SEP-2002) Genome Analysis, Institute of Molecular Submitted (10-SEP-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany

A (bases 1 to 122029)

Signature of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany

Longamann, D. and Plazzer, M.

Submitted (19-NOV-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany

On Nov 19, 2002 this sequence version replaced gi:22773267.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 122029)
Blechschmidt, K., Schattevoy, R., Baumgart, C. and Rosenthal, A.
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92
                                                                                               7.193. .27364
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/note="LiM4 repeat: matches 5646. .6154 of consensus" 27865. .27900
/note="LiM4 repeat: matches 2273. .2309 of consensus" 27901. .28132
27901. .28032
27937. .28080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF212832 122029 bp DNA linear PRI 19-NOV-
Homo sapiens chromosome 8 clone CTC-806C5 map 8q24.3, complete
   consensus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 CGATCTCCTGACCTCGTGATCCGCCCGCCTCAGCTTCCCAAAGTGCTGGGATTACAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center code: IMB
Web site: http://genome.imb-jena.de/
Contact: gecj-jeubnitegenome.imb-jena.de/
Contact: gecj-jeubnitegenome.imb-jena.de
Contact: project Information
Center project Information
Center project name: H283
Center clone name: CTC-806C5
Center clone name: TCC-806C5
Sequencing vector: pUC18; 100% of reads
Sequencing vector: pUC18; 100% of reads
Assembly program: Phrap, version 0.990329
Consensus quality: 121876 bases at least Q40
Consensus quality: 121877 bases at least Q30
Consensus quality: 121979 bases at least Q20
Quality coverage: 10.81x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 45454;
   .2765 of
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                                                                                                                                                                                                                                                                                                                                                                                                                 /note="9 copies 16 mer 63% conserved" complement(28031, .28412) /note="match: GSS: Em:AZ001959"
/note="L1M4 repeat: matches 2448.
complement(26705, .26933)
/note="match: GSS: Em:AQ245856"
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100.0%; Pred. No. 2.7e-21;
tive 0; Mismatches 0;
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0

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116766 CGATCTCCTGACCTCGTGATCCGCCCCCCTCAGCTTCCCAAAGTGCTGGGATTACAGGC 116708
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens BAC clone RP11-279K24 from 4, complete sequence. ACL04070 AC068461
AC104070.3 GI:20279508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                  /replace="G"
complement(16863..16987)
complement(63278..63368)
/note="single stranded/single chemistry region"
complement(63278..63368)
/note="single clone coverage"
complement(63298..63300)
complement(63198..63321)
complement(63323..63321)
complement(63328..63321)
complement(63334..63348)
63365
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complement (77835.77950)
complement (77835.77950)
complement (77817.79198)
complement (79147.79198)
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complement (79513.79531)
/note="single clone coverage"
complement (79518.79520)
/note="low quality region"
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/note="single stranded/single chemistry region"
63370. .63381
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complement(6327. .63536)
foote="single stranded/single chemistry region"
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/note="single stranded/single chemistry region"
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                                                                                                                                                                                                                                                                                                   'note="A substituted in clone: GS1-180I23"
                                                                                                                    note="C substituted in clone: GS1-180I23"
                                                                                                                                                                                                                               note="A substituted in clone: CTC-806C5"
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                                                       /note="A substituted in clone: CTC-806C5"
/replace="C"
                                                                                                                                                                                note="T substituted in clone: CTC-806C5"
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'note="deleted in clone: GS1-180I23"
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| Similarity 100.0%; Pred. No. 2.8e-21;
59; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                 /replace="G"
6828
                                                                                                                                        replace="T"
                     replace=""
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Best Local S:
Matches 59
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ACCESSION
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KEYWORDS
SOURCE
ORGANISM
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AC104070
LOCUS
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              This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeates; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                          Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="T substituted in clone: GS1-180123"
'replace="C"
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replace="A"
(699
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replace="G"
!956
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/replace="A"
4097
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/replace="T"
4357
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replace="C"
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replace="C"
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'replace="C"
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                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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/db_xref="taxon:9606"
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/replace="T"
                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .122029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'clone="CTC-806C5"
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REFERENCE AUTHORS

REFERENCE AUTHORS TITLE JOURNAL

REFERENCE AUTHORS JOURNAL COMMENT

JOURNAL REFERENCE

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Direct Submission
Submitted (29-MAY-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Apr 24, 2002 this sequence version replaced gi:18030153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (03-DEC-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (24-APR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mapping information for this clone was provided by Dr. John D. Merbherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P.Y., Ihao, B., Frengen, B., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Washington University Genome Sequencing Center
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                  Desai,A., Kozlowicz,A. and Boyer,E.
The sequence of Homo sapiens BAC clone RP11-279K24
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                              Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: H_NH0279K24
Drafting Center: WIBR
                     1 (bases 1 to 123291)
Sulston, J.E. and Waterston, R.
                                                                                                                                                                                                                                     (bases 1 to 123291)
                                                                                                                                                                                                                                                                                                                                                                        3 (bases 1 to 123291)
Waterston, R.H.
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Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MO 63108,
                                                                                           TITLE
JOURNAL
MEDLINE
                                                                                                                                                                                             PUBMED
REFERENCE
AUTHORS
TITLE
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TITLE
JOURNAL
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The clone sequenced to the left is RP11-45120, 2000 bp overlap; the clone sequenced to the right is RP11-173M11. Actual start of this clone is at base position 108871 of RP11-45120; actual end is at base position 123291 of RP11-279K24.

NEIGHBORING SEQUENCE INFORMATION:

VECTOR: pBACe3.6

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Unresolved tandem repeats exist between 44681 and 46316.
Polymorphisms exist between AC096659, AC0110771 and AC104070. Data
from AC110771 was used to finish AC104070.
                                                    The sequence of AC068461 has been incorporated into AC104070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reuz, .14883
rpt_family="CT-rich"
5149, .1522A
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/clone lib="RPCI-11"
174. .350
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//opt_family="ERV1"
                                                                  Location/Qualifiers
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2938. .3252
/rpt_family="Alu"
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5221. .15419
                                                                                                                                                                                                                                                                                                                                                     y="ERV1"
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739. .8079
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1345. .4522
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6357. .16729
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525_ sie
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469. .5535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         family="Malk"
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866. .6417
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2482. .12789
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2790. .12814
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535. .7724
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4307, .14427
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                                                                                                                                                                                                                                                                           .y="L2"
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269_ 5247
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Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 147613 bases at least Q40
Consensus quality: 147851 bases at least Q20
Consensus quality: 148031 bases at least Q20
Insert size: 1488563; sum-of-contigs
Insert size: 148899; 19.7% error; agarose-fp
Quality coverage: 24.62x in Q20 bases; sum-of-contigs Quality
coverage: 25.09x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * NOTE: This is a 'working draft' sequence. It currently consists of 5 conigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence is as soon as it is available and the accession number will be preserved.
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2277 2376: gap of 100 bp
2377 35686: contig of 33310 bp in length
35787 51488: contig of 15699 bp in length
51586 13546: contig of 16699 bp in length
51586 13546: contig of 80961 bp in length
13547 132646: gap of 100 bp
132647 148963: contig of 16317 bp in length
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ilarity 100.0%; Pred. No. 2.9e-21;
Conservative 0; Mismatches 0;
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1. 148963
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Amol_type="genomic DNA"
Ab_xref="taxon:9606"
chromosome="1"
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fragment_chain:1"
51586. 132546
/note="assembly_fragment:03347
fragment_chain:1"
132647. 148963
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fragment chain:1
clone_end:T7
vector_side:right"
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fragment chain:1"
35787. "51485
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Web site: http://www.sanger.ac.uk
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Homo sapiens chromosome 1 clone RP11-38J22, WORKING DRAFT SEQUENCE,
Exerging pieces.
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 148963)
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Submitted (30-JUL-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
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                                                                                                                                                                                                                                                                                9564. .19640
rpt_family="GA-rich"
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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7rpt_family="11"
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rpt family="Alu"
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7030. .17494
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AUTHORS
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE JOURNAL REFERENCE AUTHORS

REFERENCE

LOCUS DEFINITION

RESULT 15 AC012440

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4447 4546: gap of 100 bp
5801 contig of 1254 bp in length
5801 6771: contig of 871 bp in length
6772 6871: gap of 100 bp
6872 8692: gap of 100 bp
8693 11437: contig of 1745 bp in length
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87840 contig of 8398 bp in length
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8787 158619: contig of 35033 bp in length
8787 158619: contig of 35033 bp in length
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Saldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brereira, P., Castle, A., Collins, S., Collins, S., Collins, C., Cooke, P., Dehrellano, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FittHugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Grand, C., Kann, L., Karatas, A., Horton, L., Howland, J.C., Cardynson, S., Grand, C., Kann, L., Karatas, A., Horton, L., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marguis, N., McEwan, P., McEwan, P., McKernan, K., McMaughlin, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Domell, P., Peterson, K., Pollara, V., Rilara, V., Ribramanian, A., Talams, J., Stojanovic, N., Subramanian, A., Talams, J., Stojanovic, N., Subramanian, A., Talams, J., Stojanovic, N., Subramanian, A., Talams, J., Wan, X., Waman, D., Ye, M.J., Zimmer, A. and Zody, M.

Submitted (27-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, Ma 02141, USA

On Mar 1, 2000 this sequence version replaced gi:6136376.

All repeats were identified unsing RepeatMasker:
Smit, A., K. Green (1959-1997)

Mat 1, 2000 this sequence version replaced gi:6136376.

All repeats were identified unsing RepeatMasker:
Smit, A., K. Green washington.edu/RM/RepeatMasker:
Center code: Whitehead Institute/MIT Center for Genome Research
Center code: Whitehead Institute and Contact: sequence submissions@enome.wi.mit.edu

Contact: sequence submissions@enome.wi.mit.edu

Contact: sequence submissions@enome.wi.mit.edu

Contact: sequences undistitute/Species at least Q30

Consensus quality: 149892 bases at least Q30

Consensus quality: 156029 bases at least Q30

Consensus quality: 156029 bases at least Q30

Consensus quality: 156029 bases at least Q30
                                                                                                                                                                                                         AC012440 159619 bp DNA linear HTG 01-MAR-2000 mome sapiens clone RP11-11H11, WORKING DRAFT SEQUENCE, 21 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 159619)
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Insert size: 157619; sum-of-contigs
Quality coverage: 4.7 in Q20 bases; agarose-fp
Quality coverage: 4.9 in Q20 bases; sum-of-contigs
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gap of 100 bp
contig of 1693 bp in length
gap of 100 bp
contig of 1428 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Birmen, B., Linton, L., Musbaum, C. and Lander, E. Homo sapiens, clone RP11-11H11
Unpublished
(bases 1 to 159619)
                                                                                                                                                                                                                                                                                                                                        AC012440
AC012440.2 GI:7137115
HTG: HTGS PHASE1; HTGS_DRAFT.
HOMO sapiens (human)
Homo sapiens
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1225:
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TITLE JOURNAL

COMMENT

Query Match
6.0%; Score 59; DB 2; Length 159619;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 49 GṛGAṬCCGCCGCCṬCCCAAAGTGCṬCGCAGCGCACCGCGCC 107

qq

Search completed: July 10, 2004, 14:37:04 Job time : 4191 secs

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TYPE: DNA
CORGANISM: Homo sapiens
US-09-621-976-15373
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990
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-567-841A-43

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             682709 segs, 277475446 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Listing first 45 summaries
                                                                                                                         OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                    OLIGO_NUC
Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database :
                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
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Sequence 20, Appl	Seguence 3, Appli	Sequence 2, Appli	Seguence 3, Appli	Seguence 3, Appli	Seguence 15130, A		Sequence 10, Appl	٠,	Seguence 10, Appl	Sequence 7, Appli	Sequence 4, Appli	Sequence 6, Appli	Seguence 1, Appli	Seguence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 16, Appl	
US-10-067-443-20	US-09-751-389-3	US-09-110-116-2	US-09-820-002-3	US-09-984-890-3	US-09-621-976-15130	US-09-621-976-15688	US-08-257-963B-10	US-08-367-841A-10	PCT-US95-07201-10	US-09-078-294-7	US-08-520-373D-4	US-08-370-975B-6	US-08-370-975B-1	US-09-851-896-3	US-09-741-150-3	US-10-160-187-3	US-09-128-155-16	
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14364	786431	3350	21784	75395	421	438	7210	7210	7210	11811	14581	20303	26764	70000	112132	112132	152331	
4.3	4.3	4.2	4.2	4.1	0.4	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	0.4	4.0	
43	43	42	42	41	40	40	40		40	40	40	40	40		40	40	40	
28	29	30	31	32	33	34	35	36	37	38	9	40	41	42	43	44	45	
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ALIGNMENTS

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US-09-49-585-32

US-09-49-585-32

SEQUENCE 12, Application US/09497855A

PAPLICATURY: Halang TIM

MAPLICATURY: Halang TIM

TITLE OF INVENTIOR: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION

FILE REFERENCE: UNCL5.2

CURRENT APPLICATION NUMBER: 60/10.592

PRIOR APPLICATION NUMBER: 60/10.592

PRIOR APPLICATION NUMBER: 60/118,760

PRIOR APPLICATION NUMBER: 60/118,760

PRIOR APPLICATION NUMBER: 60/118,760

MACHER OF ESQ ID NOS: 1999-02-06

SOUTHWARE: Patentin version 3.0

SOUTHWARE: Patentin version 3.0

SOUTHWARE: Patentin version 3.0

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SOUTHWARE: Patentin version 3.0

SOUTHWARE: Patentin version 3.0

SOUTHWARE: Patentin version 3.0

SOUTHWARE: Patentin version 3.0

SOUTHWARE: Patentin version 3.0

SOUTHWARE: Patentin version 3.0

SOUTHWARE: Patentin version 3.0

APPLICATION NUMBER: 0.0

APPLICANT: UNDER MILE EDWARTON: ESTS and Encoded Human Proteins.

PILE REPRESENCE: GENERAL: 0.4

PAPLICANT: UNDER: 19335

CURRENT FILEND DATE: 2000-07-21

SOUTHWARE: Patentin Patentin Version 0.0

MACHER PATENT: SOUTHWARE: Patentin Version 0.0

MATTER: 19335

SOUTHWARE: Patentin Version 0.0

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APPLICANT: Crader, Gerald J.; Rodriguez,
APPLICANT: Ignacio R.; Mazuruk, Krzysztof;
APPLICANT: Ignacio R.; Mazuruk, Krzysztof;
APPLICANT: Ignacio R.; Mazuruk, Krzysztof;
APPLICANT: Tombran-fink, Joyce
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan
STREET: 345 Park Avenue
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: 3.3 kb PCR product
OTHER INFORMATION: using primers, SEQ ID No. 6319687 15 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/367,841A
FILING DATE: 30-DEC-1994
CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-UN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 174-SEP-1992
ATTOMEN'AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264126US2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                        Sequence 12, Application US/08367841A Patent No. 6319687 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 3267 Base Pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 10154
US-08-367-841A-12
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Matches
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                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Chader, Gerald J.; Becerra, S.
APPLICANT: Patricia; Schwartz, Joan P.;
APPLICANT: Patricia; Schwartz, Joan P.;
APPLICANT: Tanhwaki, Takayuki
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION OF ITS NOVEL
TITLE OF INVENTION: BIOLOGICAL ACTIVITY AND SEQUENCES ENCODING
TITLE OF INVENTION: AND EXPRESSING THE PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: 3.3 kb PCR product
OTHER INFORMATION: using primers, SEQ ID No. 5840686 15 and 16
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Query Match 4.6%; Score 46; DB 4; Length 506; Best Local Similarity 100.0%; Pred. No. 1.2e-10; Matches 46; Conservative 0; Mismatches 0; Indels
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4.5%; Score 45; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
Matches 45; Conservative 0; Mismatches 0;
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FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/552,796
FILING DATE: 24-SEPT-1992
ATTORNBY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 3643
REFERENCE/DOCKET NUMBER: 20264126US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 75-6490
TELEFAN: (212) 75-649
INFORMATION FOR SEQ ID No: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 3267 Base Pairs
TELENGTH: 3267 Base Pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WONDERFESCT 5.1
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/257,963B
                                                                                                                                                                                                                                                                                 Sequence 12, Application US/08257963B Patent No. 5840686 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Morgan & Pinnegan
STREET: 345 Park Avenue
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: Genomic DNA
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NAME/KEY: JT109
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US-08-257-963B-12
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4.5%; Score 45; DB 4; Length 3267; 100.0%; Pred. No. 2.8e-10; Live 0; Mismatches 0; Indels
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                                                                                                                                                                  625 receaaagrecressarracassearsasceaececesses 669
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Chader, Gerald J.; Becerra, Sofia
APPLICANT: Particia; Schwartz, Joan P.;
APPLICANT: Takayuki
TITE OF INVENTION: PIGMENT EPITHELIUM
                                                                                                                                                                                                                                                                           PCT-US95-07201-12; Sequence 12, Application PC/TUS9507201; GENERAL INFORMATION:
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625 receaaagreeressarracasseareasceaesseseseses

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APPLICANT: Chader, Gerald J
APPLICANT: Chader, Gerald J
APPLICANT: Becerra, Schia P
APPLICANT: Johnson, Lincoln v
APPLICANT: Rodriguez, Ignacio R
APPLICANT: TITLE OF INVENTION: REINAL PIGMENTED EPITHELIUM DERIVED NEUROTROPIC FACTOR FILE REPERENCE: 2026-4203US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
TITLE OF INVENTION: DERIVED FACTOR; CHARACTERIZATION GENOMIC TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE NUMBER OF SEQUENCES: 43
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: New York
COUNTRY: USA
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OTHER INFORMATION: 3.3 kb PCR product
OTHER INFORMATION: using primers, SEQ ID No: 15 and 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/08/520,373D
                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Floppy Disk
COMPUTER: Floppy Disk
COMPUTER: TIBN PC COMPATIBLE
OPERATING SYSTEM: PC-DOSKMS-DOS
SOFTWARE: WORDFREECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/USS5/07201
FILING DATE: 06-JUN-1995
CLASSIFICATION NUMBER: 08/367,841
FILING DATE: 30-DC-1994
FILING DATE: 07-JUN-1994
FILING DATE: 07-JUN-1994
FILING DATE: 30-DC-1994
REGISTRATION NUMBER: 34-3614
REGISTRATION NUMBER: 20264126PCT
TELECOMMINICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20264126PCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (212) 758-4800
TELEPRAX: (212) 71-6649
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 3267 Base Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Tombran-Tink, Joyce
APPLICANT: Steele, Fintan R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Unknown
MOLECULE TYPE: Genomic DNA
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US-08-520-373D-5
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Gaps
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APPLICANT: Ignacio R.; Mazuruk, Krzysztof;
APPLICANT: Ignacio R.; Mazuruk, Krzysztof;
APPLICANT: Indobran-Tink, Joyce
TITLE OF INVENTION: DIGKENT EPITHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: EXON 35-161; EXON 1142-1297; EXON 1984-2187; OTHER INFORMATION: EXON 8170-5255; INTRON 162-1141; INTRON OTHER INFORMATION: 1298-1983; INTRON 2188-5169; CDS 35-161; CDS OTHER INFORMATION: 1142-1297; CDS 1984-2187; CDS 5170-5255
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4.5%; Score 45; DB 4; Length 5262;
Best Local Similarity 100.0%; Pred. No. 2.7e-10;
Matches 45; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 TCCCAAAGTGCTGGGATTACAGGCATGAGCCACCGCCCCGGCCC 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | NAME/KEY: intron
| LOCATION: (1298)..(1983)
| NAME/KEY: intron
| LOCATION: (2188)..(5169)
| OTHER INFORMATION: n = a or g or t or c, any base
| US-08-520-373D-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/367,841A
FILING DATE: 30-DEC-1994
CURRENT FILING DATE: 1995-08-29
PRIOR APPLICATION NUMBER: 08/377,710
PRIOR FILING DATE: 1995-01-25
PRIOR FILING DATE: 1995-01-25
PRIOR FILING DATE: 1994-07-25
PRIOR PADICATION NUMBER: 07/894,215
PRIOR PADICATION NUMBER: 07/894,215
PRIOR PILING DATE: 1992-06-04
PRIOR FILING DATE: 1992-09-24
NUMBER OF SEQ ID NOS: 34
SOOFWARE: Patentin Ver: 2.1
SEQ ID NO 5
LENGTH: 5262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
US-08-367-841A-43
Sequence 43, Application US/08367841A
Patent No. 6319687
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        345 Park Avenue
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: exon
LOCATION: (1142)..(1297)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: exon
LOCATION: (1984)..(2187)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: exon
LOCATION: (5170)..(5256)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (35)..(160)
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: intron Target (162).
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                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: exon
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TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Pl-147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT-US95-07201-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-875-223-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Becerra, Sofia
APPLICANT: Chader, Gerald J.; Becerra, Sofia
APPLICANT: Taniwaki, Takayuki
TITLE OF INVENTION: PIGMENT EPITHELIUM
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDENTIFICATION METHOD:
OTHER INFORMATION: full length genomic
OTHER INFORMATION: sequence for PEDF plus flanking sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 4.5%; Score 45; DB 4; Length 22481; Best Local Similarity 100.0%; Pred. No. 2.5e-10; Matches 45; Conservative 0; Mismatches 0; Indels
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PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-UN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTONNEY/AGENT INPORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DOCKTHY R. AUTH
REGISTRATION NUMBER: 20264126US2
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION OF 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 22401 BASE PAIRS
TYPE: NUMCleic Acid
TYPE: NUMCleic Acid
TYPE: NUMCleic Acid
TYPE: NUMCleic Acid
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FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRICE APPLICATION DATA:
APPLICATION NUMBER: 08/367,841
FILING DATE: 30-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN-1994
PRICR APPLICATION NUMBER: 07/952,796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: ISM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: Unknown MOLECULE TYPE: Genomic DNA
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PCT-US95-07201-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-367-841A-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
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PETING DATE: 34-S2P-1392.

ATTAMEN CORDET NAME: 24-S2P-1392.

RANGE FORCATY RANGE: 36-S49

REFERENCE/DOCKET NAMES: 22-S4126PT

REFERENCE/DOCKET NAMES: 22-S4126PT

TELESTHON: (212) 75-S440

TELESTHON: (212) 75-S440

TELESTHON: (212) 75-S440

TTELESTHON: (212) 75-S4
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4.4%; Score 44; DB 4; Length 164;
100.0%; Pred. No. 9.2e-10;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 TCCCAAAGTGCTGGGATTACAGGCATGAGCCACCGCGCCCGGCC 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 TCCCAAAGTGCTGGGATTACAGGCATGAGCCACGGGCCGGGCC 16
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  Sequence 11863, Application US/09621976
Patent No. 663063
GENERAL INFORMATION
APPLICANT: Under Mile Edwards, J.B.
APPLICANT: Glockano, J.Y.
TITLE OF INVENTION: BSTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT FAPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 11863
LENGTH: 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Jobert, S. APPLICANT: Jobert, S. APPLICANT: Giordano, J.Y. TITLE OF INVENTION: BESTS and Encoded Human Proteins. FILE REPERENCE: GENSET, 054PR2 CURRENT APPLICATION NUMBER: US/09/621,976 CURRENT FILING DATE: 2000-07-21 NUMBER OF SEQ ID NOS: 19335 SOFTWARE: Patent.pm SEQ ID NO 1944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: sig_peptide
LOCATION: 34. 189
CHER INFORMATION: Von Heijne matrix
CTHER INFORMATION: score 3.79999995231628
CTHER INFORMATION: seq_LGAVAGACSPSCS/GG
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Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Glordano, J.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
US-09-621-976-1944/c
Sequence 1944, Application US/09621976
Patent No. 6639663
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-11863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: CDS
LOCATION: 34..195
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Sequence 2, Application US/09875114

Patent No. 6670333

GENERAL INFORMATION:
APPLICANT: No. 6670331 Bouck
APPLICANT: No. 6670331 Bouck
APPLICANT: Dow. 6670331 Bouck
APPLICANT: David Dawson
APPLICANT: Paul Gillis
TITLE OF INVENTION: Methods and Compositions for Inhibiting Angiogenesis
TITLE PERERENCE: 0290-23U2
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US/09/875,114
CURRENT FILING DATE: 1998-07-23
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1997-07-23
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH. 22484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: YAN, Chunhua et al.

APPLICANT: YAN, Chunhua et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

FILE REPERRNCE: CL001306

CURRENT APPLICATION NUMBER: US/09/984,890

CURRENT FILITG DATE: 2001-10-31

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0
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4.5%; Score 45; DB 4; Length 75395;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 45; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 4.5%; Score 45; DB 4; Length 22484; Best Local Similarity 100.0%; Pred. No. 2.5e-10; Matches 45; Conservative 0; Mismatches 0; Indels (
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CCATION: 1...22484

CTHER INCRATION: "n" means either a, c, t, or g

0S-02-875-11H-02
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LCCATION: (1)...(75395)
CTHER INFORMATION: n = A,T,C or G
US-09-984-890-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-984-890-3/c
; Sequence 3, Application US/09984890
; Patent No. 6492156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
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LENGTH: 75395
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4.4%; Score 44; DB 4; Length 294;
Best Local Similarity 100.0%; Pred. No. 8.8e-10;
Matches 44; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1940, Application US/09621976

Batent No. 6639063

GENERAL INPORMATION:

APPLICANT: Johns Milne Edwards, J.B.

APPLICANT: Johns Milne Edwards, J.B.

APPLICANT: Gloradano, J.Y.

TITLE OF INVENTION: ESTS and Encoded Human Proteins.

FILE REFERENCE: GENSET.054PR2

CURRENT APPLICANTION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SEQ ID NO 1940

IENGTH: 294
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 05.0P.R.
CURRENT APPLICATION WIMBER: US/09/621,976
CURRENT APPLIANG DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SSOFTWARE: Patent.pm
LENGTH: 294
                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: CDS
LOCATION: 34..195
NAME/KEY: sig_peptide
LOCATION: 34..186
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 3.7999995231628
OTHER INFORMATION: seq LGAVAGACSPSCS/GG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:

NAME/KRY: CDS

LOCATION: 34..195

NAME/KRY: sig peptide

LOCATION: 34..189

OTHER INFORMATION: SCORE 3.7999995231628

CHER INFORMATION: Seq LGAVACACSPSCS/GG

US-09-621-976-1940
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ORGANISM: Homo sapiens
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US-09-621-976-1940/c
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Search completed: July 10, 2004, 15:30:57 Job time : 103 secs

Prokaryot Human MLP Rhizobium

AiDS/hepa Tuberculi

Scoring table: Perfect score: Sequence:

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OM protein

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           Aah49630 |
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Aaa65458 Porcine B
Aca23355 Prokaryot
Aaf12681 Aspergill
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                                                                                                                  July 13, 2004, 08:38:15 ; Search time 375 Seconds (without alignments) 894.954 Million cell updates/sec
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                       GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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(UYCA-) UNIV CASE WESTERN RESERVE

Score

Result 8 45070

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Database:

Sutton A;

Σ,

Montano

Tang YT;

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The invention relates to isolated polymucleotide (I) and polypeptide (II) cas useful as hybridisation probes, polymerase chain recordin (FCR) primers, oligomers, and for chomosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed corivity of (II) as useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of polypeptide and polymucleotide sequences have applications in polypeptide and polymucleotide sequences have applications in diagnostics for generating equences have applications in diagnostics for generating disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic conding sequences. AAS64197-AAS94564 represent novel human diagnostic conding sequences. AAS64197-AAS94564 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in the way of the invention and the printed specification, but was obtained in the way way and the and produces are appear in the printed specification, but was obtained in the way and sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetCysGlyArgProArgArgValSerAlaGlyCysGlyPheAlaAspAlaHisTrpThr
                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone pMptb #48, 36K antigen, detection, Mycobacteria, diagnosis, infection, Crohn's disease, sarcoidosis, serological diagnosis, vaccine development, ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP; 97 A; 217 C; 196 G; 87 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 4844; 103pp; English.
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P-PSDB; ABG04853.
                                                                        Liu C,
            (HYSE-) HYSEQ INC.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                    The invention relates to a ERCoA3 (Estrogen Receptor Coregulator 3) protein and encoding polynucleotides. ERCoA3 can be used to inhibit or reduce tamoxifen or estrogen induced proliferation of cancer cells, by reduced activity of ERCoA3, and for detecting cancer cells that are ERCoA3 in cells. The encoding polynucleotide can be used to inhibit translation of a mRNA encoding ERCoA3. ERCOA3 acts as a coregulator protein and can bind to the estrogen receptor to activate a molecular or cellular response in the cell. The present sequence represents the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 AIGTGTGGGGAACGCGTGGGTAAGCGCTGGATGTGGCTTCGCTGATGCACATTGGACC 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyLeuTrpThrGlyLeuGlyGluGlyGluGlyGlylleGlyProGluGlyGlhAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerProThrProAspCysAlaSerArgTrpProArgSerAlaSerArgTrpProTrpSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AlaGlyLeuThrValArgAspArgProGlnLeuGlyGluLeuCysMetGlyArgGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 990 BP; 189 A; 281 C; 317 G; 203 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding novel human diagnostic protein #4844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-972-032-2 (1-79) x ABL60606 (1-990)
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                                                                                                                                                                                                                                  Claim 5; Fig 1; 39pp; English.
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79.00
100.00%
100.00%
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23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAR-2001; 2001WO-US008631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERCOA3 encoding cDNA
WPI; 2002-454492/48.
P-PSDB; ABB08035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200175067-A2
                                                                                                                                                                             osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-OCT-2001,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263
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Length: Matches: Conservative: Mismatches:

1.01e-15 26.00 100.00% 100.00% 32.91%

Indels:

445 26

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Β,

Klinger J; Pot D, Lamson Labat I;

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The present sequence is one of 3351 sequences in a library of human polynucleotides. The library is used to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and can detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies of the polynucleotides. The probes can be used for chromosome mapping of the polynucleotides. The probes can be used for chromosome mapping of the polynucleotides and for detection of transcription levels. Ribozymes or antisense oligonucleotides can be generated. The polynucleotides and blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or monitor the efficacy of therapies and preventive interventions. The polynucleotides, polypeptides and preventive interventions. The polynucleotides, polypeptides and treat the cancers and proliferative disorders such as neoplasia, dysplasia and hyperplasia
                                                                                                                                                      Library of polynucleotides for diagnosing a cancerous state of a mammalian cell and detecting cancer, particularly of the colon or prostate, comprises 3351 human polynucleotide sequences.
                        Williams LT, Escobedo J, Innis MA, Garcia PD, Klinger J;
Kassama A, Reinhard C, Randazzo F, Kennedy GC, Pot D, Lam
Drmanac R, Crkenjakov R, Drmanac S, Dickson M, Labat I;
Leshkowitiz D, Kita D, Garcia V, Jones LW, Strache-Crain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibacterial; infection; vaccine; gene therapy; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 379 BP; 79 A; 108 C; 110 G; 82 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N. gonorrhoeae nucleotide sequence SEQ ID 487.
                                                                                                                                                                                                                              Claim 9; Page 605-606; 1046pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyProGluGlyGlnAlaSerPro 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-972-032-2 (1-79) x AAF64670 (1-379)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGCCTGAGGGACAGGCCAGTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-FEB-2002; 2002WO-IB002069.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.4
8.00
100.00%
100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fontana MR, Pizza M,
                                                                                                                  WPI; 2001-091805/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CHIR-) CHIRON SPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200279243-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABZ37949;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABZ37949,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BXIXBXBXBXBXSXXXXBXBXBXXSX
                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents the BamHI-DNA insert of the recombinant clone pMptb #48 and encodes a 36K antigen of Mycobacterium paratuberculosis. The DNA sequence and its fragments are useful as hybridisation probes and amplification primers for detecting nucleic acid specific for the genus Mycobacterium, particularly for diagnosis of infection, especially by M. paratuberculosis which has been implicated in diagnosis and for vaccine development. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                    Mycobacterium paratuberculosis protein - as genus-specific hybridisation probe for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic; gene therapy; colon cancer; prostate cancer; cancer; lung cancer; cancer detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP; 171 A; 490 C; 552 G; 185 T; 0 U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1402
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1260 GCGTCCCGTTGCCCAGATCGGCCAGT 1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47 AlaSerArgTrpProArgSerAlaSer 55
                                                                                                                                                                                      Graham DY, El-Zaatari FAK, Naser S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (1-1402)
                                                                                                                                                  (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP
                                                                                                                                                                                                                                                                                    Recombinant clone encoding new containing nucleic acid useful
                                                                                                                                                                                                                                                                                                                                                            Claim 2; Fig 5; 12pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   x AAV36085
                                                                            95US-00447965.
                                                                                                              95US-00447965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF64670 standard; cDNA; 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-2000; 2000WO-US018374
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100.00%
11.39%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.7
                                                                                                                                                                                                                                                                                                                          detecting mycobacteria.
                                                                                                                                                                                                                          WPI; 1998-398024/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHIRON CORP.
HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-972-032-2 (1-79)
                                                                                                                                                                                                                                              P-PSDB; AAW60723.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200102568-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                          23-MAY-1995;
                                                                                                            23-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JUL-1999;
02-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
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US5776692-A
                                    07-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF64670;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human;
breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
DB:
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AAF64670/c
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à

Conservative: Mismatches: Indels:

7

Length: Matches:

ы :

Monaci

WPI; 2003-058415/05

Alignment Scores:

The

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c testing the animal for the presence of a parentally imprinted

quantitative trait locus (QTL). The pig QTL is located at chromosome 2,

mapping at around position 2pl.7. Also described are: (1) an isolated

and/or recombinant nucleic acid (N1) comprising a parentally imprinted

CC QTL or its functional fragment; (2) an isolated and/or recombinant

conclude as pig selected (N2) comprising a synthetic parentally imprinted QTL derived

from at least one chromosome or its functional fragment; (3) an animal

csuch as pig selected for having desired genotypic or potential phenotypic

properties; (4) a transgenic animal comprising N1 or N2; and (5) sperm or

an embryo derived from the animal of (3) or (4). N1 or its fragment is

useful for selecting an animal destined for slaughter or a breeding

conjunt having desired genotypic or potential phenotypic properties. The

properties are related to muscle mass and/or fat deposition. The sperm or

an embryo are useful in breeding animals destined for slaughter. AAA65418

to AAA65524 represent contigs 1 to 10 and 19 to 115 which were isolated

from porcine BAC-PIGF2-1 which contains the INS and IGF2 (insulin-like

growth factor) genes. These sequences where used in an example from the

present invention for generating a reference sequence of IGF2 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antisense, ds; prokaryotic essential gene; cell proliferation; drug design; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 600 BP; 102 A; 162 C; 228 G; 108 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          365 GGCCAAGCGTCACCGACCCCTGAC 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 GlyGlnAlaSerProThrProAsp 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-972-032-2 (1-79) x AAA65458 (1-600)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prokaryotic essential gene #5012.
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         멾
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2002; 2002WO-US009107.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACA23355 standard; DNA; 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146
8.00
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                                                                                                                                                                                                                                                                                                                                                                                flanking loci in the pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2003-029926/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; ABU19485.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACA23355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACA23355/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang
Wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Also disclosed are the nucleic acid molecules encoding the proteins and antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonornhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records AB237706-AB242016 represent nucleic acid molecules of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Selecting a domestic animal for having desired genotypic properties comprises testing the animal for the presence of a parentally imprinted quantitative trait locus which is related to muscle mass and/or fat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a method (M1) for selecting a domestic animal for having desired genotypic properties. The method comprises
                                                 New protein from Neisseria gonorrheae, useful for the manufacture of a medicament for treating or preventing N. gonorrheae infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Porcine, pig; wild boar; quantitative trait locus; QTL; chromosome 2; mapping; 2p1.7; select breeding; genotype; phenotype; muscle mass; fat deposition; IGF2; insulin-like growth factor 2; ds.
                                                                                                                                                       proteins from Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                                                                                       Sequence 483 BP; 110 A; 172 C; 124 G; 77 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                      4 8 0 0 0 0
8 8
8 3
                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              442 CGTGTATCAGCAGGATGTGGTTTT 419
                                                                                                                Disclosure; Page 224; 815pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 ArgValSerAlaGlyCysGlyPhe 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              x ABZ37949 (1-483)
                                                                                                                                                         ಧ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Fig 6; 107pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Porcine BAC-PIGF2-1 contig 49.
                                                                                                                                                       present invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-EP010209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98EP-00204291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA65458 standard; DNA; 600
                                                                                                                                                                                                                                                                                                                                                                                                    119
8.00
100.00%
100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MELICA HB.
SEGHERSGENTEC NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Georges M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-431612/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYLI-) UNIV LIEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-972-032-2 (1-79)
          P-PSDB; ABP76979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200036143-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-DEC-1998;
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AAA65458;

AAA65458/ RESULT

ò 음 22-JUN-2000.

(MELI-)

deposition

Sus scrofa.

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid choosing a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated containing the vector; (3) an isolated containing the vector; (3) an isolated containing the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of agens in an operon required for challer for proliferation, or that inhibits cellular proliferation; (6) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or which each of the strains is present in a culture or collection of required for proliferation of an organism. The antisense nucleic acids are useful for the discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. prewonnia or P. aeruginosa. The present sequence is one of the target or prokaryctic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in cellectronic format directly from WIPO at:

XX
isolate candidate molecules for rational drug discovery programs
                                                       Claim 14; SEQ ID NO 11225; 1766pp; English
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Sequence 720 BP; 127 A; 259 C; 233 G; 101 T; 0 U; 0 Other; 720 0 0 0 Length: Matches: Conservative: Mismatches: Indels: Gaps: 100.00% 100.00% 10.13% 173 8.00 Best Local Similarity: Percent Similarity: Alignment Scores: Query Match:

US-09-972-032-2 (1-79) x ACA23355 (1-720)

47 AlaSerArgTrpProArgSerAla 54 84 107 GCGAGCCGCTGGCCGCGTTCGGCC g à

AAF12681 standard; cDNA; 1015 BP. AAF12681;

13-MAR-2001 (first entry)

Aspergillus oryzae EST SEQ ID NO:5204

Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma resesi; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.

Aspergillus oryzae.

WO200056762-A2

28-SEP-2000

22-MAR-2000; 2000WO-US007781

99US-00273623 22-MAR-1999; (NOVO) NOVO NORDISK BIOTECH INC. (NOVO) NOVO NORDISK AS.

Olsen PB; Clausen IG, Berka RM, Rey MW, Shuster JR, Kauppinen S,

WPI; 2000-594572/56

Monitoring differential expression of genes in filamentous fungal ce uses fluorescence-labeled nucleic acids isolated from the cells and uses fluorescence labeled nucleic acid substrate of expressed sequence tags.

Claim 88; Page 2176-2177; 3161pp; English.

The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the F cells and a substrate of expressed sequence tags (BST). The ESTS or are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the Same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microcoganisms to be improved. New genes may be discovered, of possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway engineering. Using ESTS provides several advantages over genomic or random CDNA clones including elimination of redundants ation of the microarrays based on function of the gene copy and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AAF01478 to AAF11873 represents ESTS from Aspergillus niger; AAF11873 represents ESTS from Aspergillus oryzae, and AAF11873 represents ESTS from Aspergillus result and pages and present in the present invention

Sequence 1015 BP; 222 A; 313 C; 249 G; 230 T; 0 U; 1 Other;

00000 Length:
Matches:
Conservative:
Mismatches: Indels: Gaps: 8.00 100.00% 100.00% 10.13% Similarity: Percent Similarity: Alignment Scores: Query Match: Best Local

US-09-972-032-2 (1-79) x AAF12681 (1-1015)

26 49 ArgTrpProArgSerAlaSerArg 574/c ACA25574 standard; DNA; 1035 602 ACA25574; ACA25574 RESULT ò

Antisense; ds; prokaryotic essential gene; cell proliferation; Prokaryotic essential gene #7231. drug design; gene. SXXXXXXXXXXX

(first entry)

19-JUN-2003

Burkholderia fungorum.

836 TCGAGATGGCCGAGGTCTGCCAGT 813

(first entry)

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New nucleic acid encoding mutant MLP, useful for diagnosis and treatment of myocardial disease, particularly dilatative cardiomyopathy.
                                                                                                                                                                                                                                                           MIP; human; mutation; muscle-specific promoter; cardiovascular disease; dilatative cardiomyopathy; cardiant; gene therapy; myocardial disease; sarcomer; dystrophin; cardial actin; hypertrophic cardiomyopathy; long QT syndrome; chromosome 11p15.1; promoter; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-FEB-2000; 2000DE-01004857.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-2001; 2001WO-EP001042.
                                                                   AAH48630 standard; DNA; 1037
                                                                                                                                                                                                                 Human MLP promoter fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SCHD ) SCHERING AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-483436/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200157208-A2.
                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2001.
                                                                                                                                                                   21-SEP-2001
                                                                                                                    AAH48630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Knoell R;
                       RESULT 10
AAH48630/c
                                                                     The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibite proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated or polypeptide acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of required for proliferation, or that has an activity against a biological pathway in which a proliferation or the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibitiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or strains; or (13) identifying the strains is present in a culture or collection of a crains; or (13) identifying the extent or proliferation of an organism. The antisense nucleic acids are useful for a proliferation of an organism. The antisense nucleic acids are useful for a proliferation of an organism. The antisense nucleic acids are useful for a proliferation of an organism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         drug discovery programs, or for screening homologous mucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumonnae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                      Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 A; 290 C; 306 G; 204 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                           Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                           Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 14; SEQ ID NO 13444; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           directly from WIPO at
                                                                                                                                                                                                                                                                                                                                           Malone C,
Carr GJ,
                                                                                                                                           21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
26-CCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
                                                                                          21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                              06-MAR-2002; 2002US-0362699P
                                                                                                                                                                                                                                                                                            (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                             Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                 2003-029926/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1035 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; ABU21704
WO200277183-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                              03-OCT-2002
                                                                                                                                                                                                                                                                                                                                           Wang L,
Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                      WPI:
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This invention describes a novel nucleic acid (I) encoding an MLP (not defined) which has a 1273 base pair (bp) sequence (I) that includes a mutation at base 10 in exon 2 or the third position of codon 112 in exon 4, is new. The product of the invention has cardiant activity and can be used for gene therapy. (I), and related nucleic acids or probes, are used in diagnosis of and/or screening for mycardial diseases (or probes, are used predisposition), especially dilatative cardiomyopathy. Both specified mutations are associated with development of these diseases. Antibodies (Ab) raised against MCP and other peptides encoded by (I) can be used similarly. Also the regulatory region (III) of the genomic MLP sequence (optionally when incorporated into vectors or cells) is used in gene cherapy, specifically for prevention and/or treatment of cardiovascular disease, particularly those which involve a point mutation in a gene encoding sarcomer, dystrophin or cardial actin, e.g. hypertrophic cardiomyopathy. Into green provides muscle specific gene regulatory region of the MLP gene provides muscle specific gene regulatory region of the MLP gene provides muscle specific gene regulatory region of the MLP gene provides muscle specific gene cardiomyopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1037 BP; 285 A; 232 C; 232 G; 288 T; 0 U; 0 Other;
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8
0
0
0
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            910 CTGGGGAAGGGCAGGAGGGAGGC 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-972-032-2 (1-79) x AAH48630 (1-1037)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 LeuglyGluGlyGluGlyGly 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            numan MLP described in the invention
Claim 35; Page 51; 53pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242
8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local
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US-09-972-032-2 (1-79) x ACA25574 (1-1035)

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Length:
Matches:
Conservative:
Mismatches:
Indels:

242 8.00 100.00% 100.00%

Best Local Similarity: Query Match:

Percent Similarity

US-09-972-032-2 (1-79) x ABQ73845 (1-1230)

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The present invention describes an isolated phytase protein (I). (I) can be used for improving the nutritional value of a phytate-containing todstuff, by contacting the phytate-containing foodstuff with (I), where the enzyme catalyses the liberation of inorganic phosphate from the phytate-containing foodstuff, and so improving the nutritive value of the contacted foodstuff. The liberation of inorganic phosphate occurs prior to or after the ingestion of phytate-containing foodstuff by a recipient or producing an animal feed, by transforming a plant, plant portion or plant cell with a nucleic acid expression vector, comprising (II), culturing the plant, plant portion or plant cell with a nuclein is expressed and converting the plant, plant portion or plant cell into a composition suitable for animal feed. The animal is preferably a monogastric animal or a ruminant. (I) and (II) are useful in commove excess phytate from the environment or a sample. (I) reduces the environment. The present sequence encodes a phytase from the present
                                                                                                                                 Rhizobium; phytase; enzyme; E.C.3.1.3.8; phytate; foodstuff; feed; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel recombinant phytase protein and polynucleotide for improving nutritional value of phytate-containing foodstuff, in animal feed a feed supplements and to degrade excess phytase from environment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barton N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Richardson T, Robertson D,
                                                                                                 Rhizobium phytase nucleotide sequence SEQ ID NO:7.
                                                                                                                                                                                                                                  1. .1230
/*tag= a
/EC_number= "3.1.3.8"
/product= "phytase"
                                                                                                                                                                                                                    Location/Qualifiers
ABQ73845 standard; DNA; 1230 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 5G; 208pp; English.
                                                                                                                                                                                                                                                                                                                                                                                     12-DEC-2001; 2001WO-US048774.
                                                                                                                                                                                                                                                                                                                                                                                                                     12-DEC-2000; 2000US-0255090P.
                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Short J, Mathur EJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DIVE-) DIVERSA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-583504/62.
P-PSDB; ABP51932.
                                                                                                                                                                                                                                                                                                                     WO200248332-A2
                                                                 08-OCT-2002
                                                                                                                                                                                  Rhizobium sp.
                                                                                                                                                                                                                                                                                                                                                     20-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention
                                 ABQ73845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sample.
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Seguence 1230 BP; 182 A; 434 C; 419 G; 195 T; 0 U; 0 Other; Length:
Matches:
Conservative:
Mismatches:
Indels: Alignment Scores:

80000

8.00 100.00% 100.00%

Percent Similarity: Best Local Similarity:

Query Match:

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid conding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) an bost cell containing the vector; (3) an isolated polypeptide for its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway required for proliferation, or that that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation or that that inhibits cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the strains is present in a culture or collection of strains; or (13) identifying the taxget of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for cellular proliferation to rosteening for homologous mucleic acids required for proliferation to rosteening for homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, cultured for proliferation in cells other than S. aureus, S. typhimurium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                           ds; prokaryotic essential gene; cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 14; SEQ ID NO 13867; 1766pp; English.
                                       725 GCAAGCCGATGGCCGAGGTCGGCT 748
  54
47 AlaSerArgTrpProArgSerAla
                                                                                                                                                                                                                                                 Prokaryotic essential gene #7654.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-2001, 2001US-00815242.
06-SEP-2001, 2001US-0094893.
25-OCT-2001, 2001US-0342923P.
08-FEB-2002; 2002US-0072851.
06-MAR-2002, 2002US-0362699P.
                                                                                                                      ACA25997 standard; DNA; 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                       (first entry)
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                      Burkholderia mallei.
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                                                                                                                                                                                                                                                                                                               drug design; gene.
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                                                                                                                                                                  ACA25997;
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Wall D,
                                                                                 RESULT 12
                                                                                                       ACA2599
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and

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The present invention describes an isolated phytase protein (1). (1) can be used for improving the nutritional value of a phytate-containing foodstuff, by contacting the phytate-containing foodstuff with (1), where the enzyme catalyses the liberation of inorganic phosphate from the phytate-containing foodstuff, and so improving the nutritive value of the contacted foodstuff. The liberation of inorganic phosphate occurs prior to or after the ingestion of phytate-containing foodstuff by a recipient organism. Nucleotide sequences (11) encoding (1) can be used for
K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yersinia pestis; phytase; enzyme; E.C.3.1.3.8; phytate; foodstuff; feed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel recombinant phytase protein and polynucleotide for improving nutritional value of phytate-containing foodstuff, in animal feed feed supplements and to degrade excess phytase from environment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barton N;
                                                                                    Other;
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                                                                                    BP; 163 A; 419 C; 480 G; 177
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ftp.wipo.int/pub/published_pct_sequences
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1. .1266
/*tag= a
/EC number= "3.1.3.8"
/product= "phytase"
                                                                                                                                                                                                                                                                                   AGCAGATGGCCGCGCAGCGCTTCA 118
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                                                                                                                                                           Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yersinia pestis.
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                                                                                      Sequence 1239
                                                                                                                 Alignment Scores:
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producing an animal feed, by transforming a plant, plant portion or plant the plant, plant portion or plant cell with a nucleic acid expression vector, comprising (II), culturing the plant, plant portion or plant cell under conditions in which the phytase protein is expressed and converting the plant, plant portion or plant cell into a composition suitable for animal feed. The animal is preferably a monogastric animal or a ruminant. (I) and (II) are useful in animal feed and feed supplements as well as in treatments to degrade or remove excess phytate from the environment or a sample. (I) reduces phytate levels in animal manure and so reduces the phosphate pollution of the environment. The present sequence encodes a phytase from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence may be used to produce a recombinant protein comprising alpha-antigen and B-cell epitope of the HIV-1 aga antigen prigon product is useful in vaccine production eg. tuberculosis. A live vaccin such as M.bovis BCG or M.smegmatis has a low toxicity and long lasting such as M.bovis BCG or M.smegmatis has a low toxicity and long lasting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New mycobacterial secretory vector - used to transform host cells, and
                                                                                                                                                                                    Sequence 1266 BP; 194 A; 444 C; 426 G; 202 T; 0 U; 0 Other;
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90JP-00064310.
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                                                                                                                                                            invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Medicinal use of Mycobacterium-originated alpha-antigen or its gene in treating allergic diseases e.g. atopic dermatitis, asthma, allergic rhinitis and allergic conjunctivitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antiallergic, Dermatological, Antiasthmatic; Antinflammatory, Ophthalmological, Mycobacterium-originated alpha antigen, allergic disease; atopic dermatitis; asthma; allergic rhinitis; allergic conjunctivitis; interleukin-4; Th2-type cytokine; IgE production; histamine; eosinophilic infiltration; gene; ss.
                                                      Sequence 1349 BP; 232 A; 434 C; 438 G; 245 T; 0 U; 0 Other;
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